

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 18:33:00 ; Search time 301 Seconds  
(without alignments)  
7578.157 Million cell updates/sec

Title: US-09-925-301-124

Perfect score: 845

Sequence: 1 ggcagaggtcacaccgcga.....gagggggggggcccccccccc 845

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
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3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.8	845	21	AACT7730 Human cancer assoc
2	758	89.7	1057	25	ACCS0321 Breast cancer asso
3	748.6	88.6	962	23	ABV29510 Human prostate exp
4	744.4	88.1	786	24	ABR25755 Human site-specific
5	735.2	87.0	748	24	ABO61087 RIKEN 181046019 p
6	705	83.4	725	22	AAI71793 Human C35 coding s
7	653.8	77.4	762	24	ABQ56132 Human ovarian anti
8	565.2	66.9	814	23	ABV23648 Human prostate exp

9	565	66.9	602	23	ABV44776 Human prostate exp
10	469	55.5	875	23	ABV14903 Human breast exp
11	400	47.3	404	22	AAH55578 Human breast tumou
12	381.2	45.1	517	23	ABV38989 Human prostate exp
13	354	41.9	354	22	AAH71785 Human C35 coding s
14	354	41.9	354	23	AAH77148 Human pancreatic c
15	346	40.9	346	24	ABV67744 Human pancreatic c
16	300	35.5	300	24	ABO78746 Differentially exp
17	299.4	35.4	301	24	ABV97310 Human pancreatic c
18	297.4	35.2	299	24	ABV69897 Human pancreatic c
19	290.2	34.3	419	16	AAI23303 Human gene signatu
20	284	33.6	285	24	ABV99124 Human pancreatic c
21	281.8	33.3	293	24	ABV97062 Human pancreatic c
22	265.8	31.5	416	25	ABX51910 Bovine EST associa
23	260.2	30.8	310	21	AAI03159 Human secreted pro
24	228.8	27.1	437	24	ABL59499 EST related to ham
25	170.6	20.2	715	24	ABV76834 Frog embryonic gen
26	168	19.9	345	23	ABV05734 Human prostate exp
27	146.2	17.3	565	22	AAI15834 Human breast cance
28	127.4	15.1	373	22	AAI24678 Human breast cance
29	98.2	11.6	340	25	ABX1896 Bovine EST associa
30	87	10.3	433	24	ABL78369 Human ovarian can
31	82.6	9.8	371	21	AAI09806 Human colon cancer
32	82.4	9.8	588	20	AAV84464 Human secreted pro
33	82.4	9.8	588	22	ABAB3247 Human secreted pro
34	78.4	9.3	1016	21	AACT8044 Human cancer assoc
35	78.2	9.3	458	23	ABV48154 Human prostate exp
36	78.2	9.3	6065	22	AAI79908 Human secreted pro
37	78.2	9.3	6066	24	ABQ54960 Human ovarian anti
38	78	9.2	985	22	AAI08199 Human secreted pro
39	78	9.2	985	22	AAI08212 Human secreted pro
40	78	9.2	1111	24	ABP10006 Human polynucleoti
41	77.6	9.2	1635	21	AAI21664 Human breast and o
42	77.6	9.2	2884	24	ABK0847 Human polynucleoti
43	77.6	9.2	2958	23	ABK43639 DNA encoding novel
44	77.2	9.1	706	24	AAI33711 Human secreted pro
45	77	9.1	1606	24	ABQ54999 Human ovarian anti

## ALIGNMENTS

RESULT 1	
AACT7730	
ID	AACT7730 standard; cDNA; 845 BP.
AC	AACT7730;
XX	08-FEB-2001 (first entry)
XX	Human cancer associated gene sequence SEQ ID NO:124.
XX	Human, cancer associated gene; cancer antigen; detection; cancer;
KW	diagnosis; cytotoxic; proliferative; vulnerrary; immunomodulator;
KW	antidiabetic; antisthmatic; antirheumatic; antiarthritic; antiviral;
KW	antiflammatory; antihypoid; antiallergic; antibacterial; cardiac;
KW	dermatological; neuroprotective; thrombolytic; coagulant; noctropic;
KW	vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW	allergic reaction; graft versus host disease; organ rejection;
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;
KW	neurological disease; drug screening; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200055350-A1.
XX	
PD	21-SEP-2000.
XX	
PF	08-MAR-2000; 2000WO-US05882.
XX	
PR	12-MAR-1999; 99US-0124270.
XX	

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI, 2000-587533/55.  
 XX P-SDB; AAB43521.  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 XX useful for treating or diagnosing e.g. cancer -  
 XX  
 PS Claim 1, Page 707-708, 2352pp; English.  
 XX  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given  
 CC in AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytoskeletal; proliferative; vunerary; immunomodulator;  
 CC antidiabetic; antistatic; antirheumatic; antitachytic;  
 CC antiinflammatory; antihypoid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antiprostatic and angiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilization of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention.  
 XX  
 XX  
 SQ Sequence 845 BP, 222 A; 235 C; 227 G; 159 T; 2 other;

Query Match 99.8%; Score 843; DB 21; Length 845;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-145;  
 Matches 845; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGAGGTTCAACCCGGAAGCGGGGCGGAGCCGGCCCGGATGAGCGGGGA 60  
 DB 1 GGCAGAGGTTCAACCCGGAAGCGGGGCGGAGCCGGCCCGGATGAGCGGGGA 60  
 QY 61 GCGGGGCGAAGCGGCGGTAGCGGCCCTCCGAGAGAGTGAGCGGGGCGGTCG 120  
 DB 61 GCGGGGCGAAGCGGCGGTAGCGGCCCTCCGAGAGAGTGAGCGGGGCGGTCG 120  
 QY 121 CATCGTGTGAGAGTGTGTAACCTTGCGGCTTGAGGCGACCTTACCTGAGCTGCGCAG 180  
 DB 121 CATCGTGTGAGAGTGTGTAACCTTGCGGCTTGAGGCGACCTTACCTGAGCTGCGCAG 180  
 QY 181 TGCTGTGAAGAGAGATCCGGGCGATCGAGATGAGTCCGGCTCGGGGGCAGAGGTGC 240  
 DB 181 TGCTGTGAAGAGAGATCCGGGCGATCGAGATGAGTCCGGCTCGGGGGCAGAGGTGC 240  
 QY 241 CTTTGAATGAGATTAAGAGACAGCTGTGTTCTCCAGCTGAGAAATGGGGCTTTC 300  
 DB 241 CTTTGAATGAGATTAAGAGACAGCTGTGTTCTCCAGCTGAGAAATGGGGCTTTC 300  
 QY 301 CTATGAGAAAGATCTATTGAGGCGCATCGAAGAGCCAGTAATGAGAAACCTTAGAAAA 360  
 DB 301 CTATGAGAAAGATCTATTGAGGCGCATCGAAGAGCCAGTAATGAGAAACCTTAGAAAA 360  
 QY 361 GATCACCAGAGCGGCTCTCCGCTGATCTGTGACTGACAGAGACTTGGGTTCTTG 420  
 DB 361 GATCACCAGAGCGGCTCTCCGCTGATCTGTGACTGACAGAGACTTGGGTTCTTG 420  
 QY 421 CTCTGTTCTGGGGGCAACCTTGTCTCTCTTGTGTCGTCGGGAGCTCCCTTGGCT 480  
 DB 421 CTCTGTTCTGGGGGCAACCTTGTCTCTCTTGTGTCGTCGGGAGCTCCCTTGGCT 480  
 QY 481 CTTTCCCTCTTAGCTCTTAGCAAGAGACCTGCGCTTCACTTGTGCTTGGGTAC 540

DB 481 CTTTCCCTCTTAGCTCTTAGCAAGAGACCTGCGCTTCACTTGTGCTTGGGTAC 540  
 QY 541 AAGAGAGAAATGAAATTCGCGGCTTGGGGCGAGAGAGACACTTCATGAACA 600  
 DB 541 AAGAGAGAAATGAAATTCGCGGCTTGGGGCGAGAGAGACACTTCATGAACA 600  
 QY 601 CTCTCCAGCAGCCTGATACCCCTTCCAGGGTAAGTCCCAAGCCAGTCCACT 660  
 DB 601 CTCTCCAGCAGCCTGATACCCCTTCCAGGGTAAGTCCCAAGCCAGTCCACT 660  
 QY 661 CTTCGCTGGTGAATACCTGTGTGATGCCACAGATTATTTATTTCTCCCTAACCCAGG 720  
 DB 661 CTTCGCTGGTGAATACCTGTGTGATGCCACAGATTATTTATTTCTCCCTAACCCAGG 720  
 QY 721 GCAATGTGAGCTTTTGGCAGTAAGTGGGCTTCAACAACCTAATAAAAAAAAAAAAAA 780  
 DB 721 GCAATGTGAGCTTTTGGCAGTAAGTGGGCTTCAACAACCTAATAAAAAAAAAAAAAA 780  
 QY 781 AA 840  
 DB 781 AA 840  
 QY 841 CCCCC 845  
 DB 841 CCCCC 845

RESULT 2  
 ACC50321  
 ID ACC50321 standard; cDNA; 1057 BP.  
 XX  
 AC ACC50321;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Breast cancer associated cDNA sequence SEQ ID NO:479.  
 XX  
 KW Human; breast cancer; cytoskeletal; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003004989-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US19669.  
 XX  
 PR 21-JUN-2001; 2001US-299887P.  
 PR 27-JUN-2001; 2001US-301572P.  
 PR 18-JUL-2001; 2001US-306501P.  
 PR 25-SEP-2001; 2001US-325002P.  
 PR 05-MAR-2002; 2002US-362585P.  
 PR 14-MAY-2002; 2002US-380391P.  
 XX  
 PA (MILL-) MILLENIUM PHARM INC.  
 XX  
 PI Lilie J, Gannavarapu M, Glatz K, Hoersch S, Kamatkar S, Mertens M;  
 PI Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE, Baet RC;  
 PI Hortobaegy I, Puzsai L, Meric F, Sahin A, Mills GB;  
 XX  
 DR WPI; 2003-210381/20.  
 DR P-SDB; ABR47619.  
 XX  
 XX  
 PT Breast cancer diagnosis or treatment by comparing the level of  
 PT expression of a marker in a patient sample with that in the control  
 PT non-breast cancer sample -  
 XX  
 PS Claim 1; SEQ ID 479; 128bp; English.  
 XX  
 CC The present invention describes a method for assessing whether a patient  
 CC is afflicted with breast cancer. The method comprises comparing the level  
 CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and



[illegible]

XX	RESULT 4
XX	ID AB225755 standard; cDNA; 786 BP.
XX	AC AB225755;
XX	AB225755;
XX	28-MAR-2003 (first entry)
XX	Human site-specific recombinase motif-containing protein 12.63 cDNA.
XX	Human, site-specific recombinase motif-containing protein 12.63;
XX	recombinant production; gene therapy; cancer; tumour; HIV infection;
XX	human immunodeficiency virus; cytosolic; gene; ss.
XX	Homo sapiens.
XX	
XX	Key location/Qualifiers
XX	38..385
XX	/*tag= a
XX	/product= "human site-specific recombinase motif-
XX	containing protein 12.63"
XX	CN1363589-A.
XX	14-AUG-2002.
XX	05-JAN-2001; 2001CN-0105072.
XX	05-JAN-2001; 2001CN-0105072.
XX	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX	
XX	Mao Y, Xie Y;

XX	WPI, 2002-742038/81.
DR	P-P8DB; ABP58560.
XX	
PT	Polypeptide-human protein 12.63 containing site-specific recombinase
PT	characteristic sequence fragment and polynucleotide for coding it -
XX	
PS	Claim 6; Page 26-27 (Disclosure); 33pp; Chinese.
XX	
CC	The invention relates to human site-specific recombinase motif-containing
CC	protein 12.63 (ABP58560) and nucleic acids encoding it (ABZ25755). The
CC	protein has a molecular weight of 12.63 kD. The invention also relates to
CC	a method for the recombinant production of the protein, an antagonist of
CC	the protein, and the use of the protein, gene and antagonist in
CC	therapeutic applications. Site-specific recombinase motif-containing
CC	protein 12.63 can be used in the treatment of a variety of diseases such
CC	as cancer and HIV (human immunodeficiency virus) infection. The present
CC	sequence represents cDNA encoding human site-specific recombinase motif-
CC	containing protein 12.63.
XX	
SQ	Sequence 786 BP; 175 A; 233 C; 220 G; 158 T; 0 other;
Query Match	88.1%; Score 744.4; DB 24; Length 786;
Best Local Similarity	99.1%; Pred. No. 8.2e-127;
Matches 759; Conservative	0; Mismatches 6; Indels 1; Gaps 1

QY	12	ACACCCGGAACAGAGGGGCCCCGAGCGGAGAGCCGGCCGCATAGCCGGAGAGCCGGGGCAGA	71
Db	1	ACACCCGGAACAGAGGGGCCCCA-GCGAGCCGGCCGCATAGACGGGAGCCGGGGCAGA	59
QY	72	CGTCGTAGGCCCCCTTCCGAGAGAGTCGAGCCGGGCAGTGGGGTCCGCATCGTGTGG	131
Db	60	CGTCGTAGGCCCCCTTCCGAGAGAGTCGAGCCGGGCAGTGGGGTCCGCATCGTGTGG	119
QY	132	AGTACTGTGAACCCCTGGAGGCTTCCAGAGGAGCACTACCTGAGCTGGCCAGTGTCTGAAG	191
Db	120	AGTACTGTGAACCTCTGGGGCTTCCAGAGGAGCACTACCTGAGCTGGCCAGTGTCTGAAG	179
QY	192	AGCAGTATCCGGGCAATCGAGATCGAGTCGGGCTTCGGGGGCAACAGTGCCTTTGAGATG	251
Db	180	AGCAGTATCCGGGCAATCGAGATCGAGTCGGGCTTCGGGGGCAACAGTGCCTTTGAGATG	239
QY	252	AGATPAAAGGACAGCTGGTGTCTCCAGAGCTGGAGAAATGGGGGGCTTCCCTATGGAAG	311
Db	240	AGATPAAAGGACAGCTGGTGTCTCCAGAGCTGGAGAAATGGGGGGCTTCCCTATGGAAG	299
QY	312	ATCTCATTTAGAGGCCATCCGAAAGGCACTGAATGGAAGAAACCTTAGAAAAAGATCAACA	371
Db	300	ATCTCATTTAGAGGCCATCCGAAAGGCACTGAATGGAAGAAACCTTAGAAAAAGATCAACA	359
QY	372	GCGGTCCTCCCTGGGTATCTCTGGACTGGACAGAGACTCTGGGTCCGTGCTGTCTTGG	431
Db	360	GCGGTCCTCCCTGGGTATCTCTGGACTGGACAGAGACTCTGGGTCTGTGCTGTCTGG	419
QY	432	GATCCAAACCTTGGTCCCTCTTTGGTCCGTGGGAGTCCCCCTGCCTCTTCCCTAC	491
Db	420	GATCCAAACCTTGGTCCCTCTTTGGTCCGTGGGAGTCCCCCTGCCTCTTCCCTAC	479
QY	492	TTAGTCTCTTAGCAAGAGACCTCGGCTCACTTGTGCTTTGGGTACAAAGAGAAAT	551
Db	480	TTAGTCTCTTAGCAAGAGACCTCGGCTCACTTGTGCTTTGGGTACAAAGAGAAAT	539
QY	552	AGAGATTCGCTGGGCTTGGGGGGCAGAGAGAGACACTCTCCATGAACACTCTCCAGCC	611
Db	540	AGAGATTCGCTGGGCTTGGGGGGCAGAGAGAGACACTCTCCATGAACACTCTCTCAGCC	599
QY	612	AACCTGATACCCCTTCCAGAGGTAAGTGCCACGAAAGCCCAAGTCACTTTCGCTGG	671
Db	600	AACCTGATACCCCTTCCAGAGGTAAGTGCCACGAAAGCCCAAGTCACTTTCGCTGG	659
QY	672	TAATACCTGTCTGATGACACAGATTTTATTTATCTCCCTTAACCAAGGCAATGTACG	731
Db	660	TAATACCTGTCTGATGACACAGATTTTATTTATCTCCCTTAACCAAGGCAATGTACG	719

QY 732 TATTGCGAGTAAGTGGCGCTACAAACACTATAAAAAAAAAAAAAA 777  
 DB 720 TATTGCGAGTAAGTGGCGCTACAAACACTATAAAAAAAAAAAAAA 765

RESULT 5  
 ABO61087  
 ID ABO61087 standard; cDNA; 748 BP.

AC ABO61087;

DT 26-FEB-2003 (first entry)

DE RIKEN 1810046J19 protein encoding sequence.

XX Neuroprotective; immunomodulator; cancer; chromosome 4q13-q21;  
 XX cytosolic; anti-inflammatory; gene therapy; nutritional supplement;  
 XX wound; burn; ulcer; Alzheimer's disease; Huntington's disease;  
 XX amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 XX vulnerability; gene; ss.

OS Homo sapiens.

PN WO200231111-A2.

PD 18-APR-2002.

PE 11-OCT-2001; 2001WO-US27760.

PR 12-OCT-2000; 2000US-0687527.

XX (HYSE-) HYSEQ INC.

PI Tang Y, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR WPI; 2002-426278/45.

XX N-PSDB; ABP43843.

XX New polypeptides and their encoded proteins, useful as nutritional  
 FT sources or supplements, or in gene therapy, particularly for treating  
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, or  
 PT inflammation

XX Claim 1; SEQ ID # 300; 357pp + sequence listing; English.

XX The invention relates to 446 newly isolated polynucleotide sequences.  
 CC The activity of polynucleotides of the invention may be described as,  
 CC vulnerability, neuroprotective, immunomodulator, cytosolic and  
 CC anti-inflammatory. Compositions comprising nucleic acids of the invention  
 CC are useful for treating a mammalian subject, or as nutritional sources or  
 CC supplements. These are useful in gene therapy, particularly for treating  
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or  
 CC inflammation. The nucleic acids and polypeptides are also useful in  
 CC diagnostic and research methods. The sequences given in records  
 CC ABO60788-ABO61233 represent polynucleotides of the invention.  
 CC NOTE: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 748 BP; 169 A; 216 C; 208 G; 155 T; 0 other;

Query Match 87.0%; Score 735.2; DB 24; Length 748;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-125;  
 Matches 740; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 28 GCCCGAGCGGAGCGCGCGGATGAGCGGGAGCGCGGAGACGTCGTAAGCGCC 87  
 DB 1 GCCCGAGCGGAGCGCGCGGATGAGCGGGAGCGCGGAGACGTCGTAAGCGCC 60  
 QY 88 TCCGAGAGAGTCCAGCGGCGAGTGGGATCCGATCTGTGTGAGTACTGGAACCTG 147

DB 61 TCCGAGAGAGTCCAGCGGCGAGTGGGATCCGATCTGTGTGAGTACTGGAACCTG 120  
 QY 148 CGGCTTCAGAGCGACCTTACTCTGAGCTGGCCAGTGTCTGTAGAGACGATTCGGGGCAT 207  
 DB 121 CGGCTTCAGAGCGACCTTACTCTGAGCTGGCCAGTGTCTGTAGAGACGATTCGGGGCAT 180  
 QY 208 CGAGATCGAGTCGGGCGCTCGGGGGGACAGTGGCTTTGAGATAGAGATTAATGACAGCT 267  
 DB 181 CGAGATCGAGTCGGGCGCTCGGGGGGACAGTGGCTTTGAGATAGAGATTAATGACAGCT 240  
 QY 268 GGTGTCTCCAGCTGAGAAATGGGGGCTTCCCTATGAGAAAGATCTCATTTAGAGCCAT 327  
 DB 241 GGTGTCTCCAGCTGAGAAATGGGGGCTTCCCTATGAGAAAGATCTCATTTAGAGCCAT 300  
 QY 328 CCGAAGAGCCGATATGAGAAACCTTAGAAAAGATACCAACAGCGCTCTCCCTGCGT 387  
 DB 301 CCGAAGAGCCGATATGAGAAACCTTAGAAAAGATACCAACAGCGCTCTCCCTGCGT 360  
 QY 388 CATCTGTGACTGACACAGGACTCTGGGTTCTGCTGTCTGTGTGAGGATCAAAACCTTGGTC 447  
 DB 361 CATCTGTGACTGACACAGGACTCTGGGTTCTGCTGTGTGTGAGGATCAAAACCTTGGTC 420  
 QY 448 TCCCTTGTCTCTGCGAGCTCCCTGCTCTTTCCCTACTTAGCTTCTTAGCAAA 507  
 DB 421 TCCCTTGTCTCTGCGAGCTCCCTGCTCTTTCCCTACTTAGCTTCTTAGCAAA 480  
 QY 508 GAGACCTCGGCTCTCACTTTGGCTTTGGGTACAAAGAGAAATGAAATTCGTGGCC 567  
 DB 481 GAGACCTCGGCTCTCACTTTGGCTTTGGGTACAAAGAGAAATGAAATTCGTGGCC 540  
 QY 568 TTGGGGGAGAGAGAGACCTCTCCATGAACATTTCTCCAGCACTCATACCCCTTC 627  
 DB 541 TTGGGGGAGAGAGAGACCTCTCCATGAACATTTCTCCAGCACTCATACCCCTTC 600  
 QY 628 CCAAGGTAGTGGCCACGAAAGCCAGTCACTCTTGGCTCGGTAAATACCTGTCTGATG 687  
 DB 601 CCAAGGTAGTGGCCACGAAAGCCAGTCACTCTTGGCTCGGTAAATACCTGTCTGATG 660  
 QY 688 CCACAGATTTTATTTATTTCTCCCTAACCCAGGCAATGTACGATTTGGCATTAAGTG 747  
 DB 661 CCACAGATTTTATTTATTTCTCCCTAACCCAGGCAATGTACGATTTGGCATTAAGTG 720  
 QY 748 GCGCTACAAACACTTAAAAA 775  
 DB 721 GCGCTACGACAAATATAAAAAA 748

RESULT 6  
 ID AAI17193  
 AC AAI17193 standard; cDNA; 725 BP.

XX AAI17193;

DT 22-JAN-2002 (first entry)

XX Human C35 coding sequence #2.

XX Human; C35; cytosolic; gene therapy; vaccine; tumour antigen; ss;  
 KW breast cancer; bladder cancer; tumour immunotherapy; chromosome 17q12.

XX Homo sapiens.

OS Homo sapiens.

Key Location/Qualifiers  
 FT CDS 22..369  
 FT /tag= a  
 FT /product= "Human C35"

PN WO200174859-A2.

XX 11-OCT-2001.

PF 04-APR-2001; 2001WO-US10855.



CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents cDNA encoding a human ovarian antigen of the  
 CC invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 762 BP; 167 A; 215 C; 210 G; 163 T; 7 other;

Query Match 77.4%; Score 653.8; DB 24; Length 762;  
 Best Local Similarity 96.9%; Pred. No. 2.6e-110;  
 Matches 677; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 26 GGGCCCGAGGCGGAGCCGGCCGATGAGCGGGGAGCCGGGCGAGAGCTCCGTACGCGCC 85  
 DB 5 GGGGCGCGGAGCGGAGCCGGCCGATGAGCGGGGAGCGGGGCGAGAGCTCCGTACGCGCC 64  
 QY 86 CCTCCCGAGAGAGTGAAGCGGGGCAAGTGGGCTCCGATCTGTGTGAGTACTGTGAACC 145  
 DB 65 CCTCCCGAGAGAGTGAAGCGGGGCAAGTGGGCTCCGATCTGTGTGAGTACTGTGAACC 124  
 QY 146 TCGGCGCTTGAGAGCGACCTGAGAGCTGCGGAGGCTGAGAGAGAGAGTCCGGGC 205  
 DB 125 TCGGCGCTTGAGAGCGACCTGAGAGCTGCGGAGGCTGAGAGAGAGAGTCCGGGC 184  
 QY 206 ATCGAGATGAGTGCAGCTCGGGGCGACAGGTGCTTGTAGATAGAGTAATGAGCAG 265  
 DB 185 ATCGAGATGAGTGCAGCTCGGGGCGACAGGTGCTTGTAGATAGAGTAATGAGCAG 244  
 QY 266 CTGCTGTCTTCCAGACTGGAATGSGGGCTTCCCTATGAGAAAGATCTCATTGAGGCC 325  
 DB 245 CTGCTGTCTTCCAGACTGGAATGSGGGCTTCCCTATGAGAAAGATCTCATTGAGGCC 304  
 QY 326 ATCCGAGAGCGCAGTATGAGAGAAACCTAGAAAAGATACCAAGCGCTCCCTCCG 385  
 DB 305 ATCCGAGAGCGCAGTATGAGAGAAACCTAGAAAAGATACCAAGCGCTCCCTCCG 364  
 QY 386 GTCATCTGTGACTGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGG 445  
 DB 365 GTCATCTGTGACTGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGG 424  
 QY 446 TCTCCCTTTGGTCTGCTGAGGAGCTCCCTGCTCTTCCCTTACCTTACTGCTTACCA 505  
 DB 425 TCTCCCTTTGGTCTGCTGAGGAGCTCCCTGCTCTTCCCTTACCTTACTGCTTACCA 484  
 QY 506 AAGAGACCTGGGCTCCGACTTGGCTTGGGTAAAGAGAGATTAAGATTCCTCTGG 565  
 DB 485 AAGAGACCTGGGCTCCGACTTGGCTTGGGTAAAGAGAGATTAAGATTCCTCTGG 544  
 QY 566 CTTTGGGGGCGAG 625  
 DB 545 CTTTGGGGGCGAG 604  
 QY 626 TCCGAGGATGAGTCCGAG 685  
 DB 605 TCCGAGGATGAGTCCGAG 664  
 QY 686 TG---CCAGAGATTTATTTATTTCTCCCTAACCAGGG 721  
 DB 665 TGCCCCGAGATTTATTTATTTCTCCCTAACCAGG 703

RESULT 8  
 ID ABV23648/c  
 XX ABV23648 standard; cDNA; 814 BP.  
 AC ABV23648;  
 XX

DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 23639.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US05171.  
 XX  
 PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 PI Schlegel R, Endege WO, Monahan JB;  
 DR WPI, 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 433-434; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX  
 SQ Sequence 814 BP; 181 A; 202 C; 231 G; 199 T; 1 other;

Query Match 66.9%; Score 565.2; DB 23; Length 814;  
 Best Local Similarity 93.4%; Pred. No. 3.7e-94;  
 Matches 622; Conservative 0; Mismatches 18; Indels 26; Gaps 2;

QY 139 TGAACCTGGGGCTTCAAGGCGACCTTACCTGAGAGCTGGCCAGTCTGTGAAGAGCGATA 198  
 DB 792 TCAACGGGGGGGGCTTGTGCGACCTTACCTGAGAGCTGGCCAGTCTGTGAAGAGCGATA 733  
 QY 199 TCGGCGATGAGATCGAGTCCGCGCTCGGGGGGACCA----- 235  
 DB 732 TCGGCGATGAGATCGAGTCCGCGCTCGGGGGGACAGGTGAGGCTCGAGAACACCTGC 673  
 QY 236 -GGTGGCTTTGAGATGAGATTAATGAGCAGCTGTGTTCTCCAAAGCTGAGAAATGGGG 293  
 DB 672 TGGGTGCTTTGAGATGAGATTAATGAGCAGCTGTGTTCTCCAAAGCTGAGAAATGGGG 613  
 QY 294 GCTTCCCTATGAGAAAGATCTATTGAGGCGCATCCGAAAGAGCAGTAATGAGAAACCC 353  
 DB 612 GCTTCCCTATGAGAAAGATCTATTGAGGCGCATCCGAAAGAGCAGTAATGAGAAACCC 553  
 QY 354 TAGAAAGATCAACCAAGCGCTCTCCCTGC-GTCATCTGTGACTGCACAGAGACTCTG 412



KW pharmacogenomic marker; gene; ss.  
 OS Homo sapiens.  
 PN MO200160860-A2.  
 XX 23-AUG-2001.  
 PD 20-FEB-2001; 2001WO-US05171.  
 PF 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 PA Schlegel R, Endege WO, Monahan JE;  
 PI MPI; 2001-662795/76.  
 DR Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX  
 PS Claim 1; Page 2496; 11750pp; English.  
 CC The invention relates to an isolated nucleic acid molecule (1) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (1) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 CC  
 CC Sequence 875 BP; 204 A; 241 C; 216 G; 210 T; 4 other;  
 XX  
 SQ  
 Query Match 55.5%; Score 469; DB 23; Length 875;  
 Best Local Similarity 84.7%; Pred. No. 1.3e-76;  
 Matches 572; Conservative 0; Mismatches 75; Indels 28; Gaps 3;  
 Oy 139 TGAACCTGCGGCTTCGAGGCGAAGCTTACCTGAGCTGCGCACTGCTGGAAGAGCACTA 198  
 Db 89 TCAAGCGCGGGGCTTCGTCGCACTTACCTGAGCTGCGCACTGCTGGAAGAGCACTA 148  
 Oy 199 TCCGGGCAATCGAGATCGAGTGGCGGCTCGGGGGGCA----- 235  
 Db 149 TTCGGGCAATCGAGATCGAGTGGCGGCTCGGGGGGCAAGGTGAGTGCATTAACACCTTCT 208  
 Oy 236 -GGTGCCTTTGAGATAGATTAATGACAGCTGCTGTTCTTCAAGCTGAGGAATGAGG 294  
 Db 209 GGGTGCCTTTGAGATAGATTAATGACAGCTGCTGTTCTTCAAGCTGAGGAATGAGG 268  
 Oy 295 CTTTCCCTATGAGAAAGATTCATTTAGAGCCATCCGAAGAGCCAGTATGAGAAACCTT 354  
 Db 269 CTTTCCCTATGAGAAAGATTCATTTAGAGCCATTCGAAGAGCCAGTATGAGAAACCTT 328  
 Oy 355 AGAAAGATTCACCAACAGCCGCTCCTCTGC-GTCATCCTGTGACTGACAGAACTTGG 413  
 Db 329 AGAAAGATTCACCAACAGCCGCTCCTCTGC-GTCATCCTGTGACTGACAGAACTTGG 388  
 Oy 414 GTTCTGCTGCTGTTGCGGGTTCAAACCTTGGTCTCCCTTGGTCTGCTGCGAGCTTCC 473

Db 389 GTTCTGCTGCTGTTTCTGCGGGTTCAAACCTTGGTCTCCCTTGGTCTGCGAGCTCCC 448  
 Oy 474 CTTGCTCTTTTCCCTTACTTACTTCTCTTACGAAAGAGACCTTGGCTTCACTTGGCCTT 533  
 Db 449 CTTGCTCTTTTCCCTTACTTACTTCTCTTACGAAAGAGACCTTGGCTTCACTTGGCCTT 508  
 Oy 534 TGGGTACAAAGAGATAGAAAGATTCCGTGCGCTTGGGGGCGAGAGAGACACTTCC 593  
 Db 509 TGGGTACAAAGAGATAGAAAGATTCCGTGCGCTTGGGGGCGAGAGAGACTTCC 568  
 Oy 594 ATGAACACTTTCAGACCCATCATACCCCTTCCAGAGGTAGTCCACAGAAAGCCCA 653  
 Db 569 ATGAACACTTTCAGACCCATCATACCCCTTCCAGAGGTAGTCCACAGAGCTCA 628  
 Oy 654 GTTCACTTTCGCTTCCGTAATACCTGCTGTAATGCGACAGATTTTATTATTCCTCTA 713  
 Db 629 GTTCACTTTCGCTTCCGTAATACCTGCTGTAATGCGACAGATTTTATTATTCCTCTA 688  
 Oy 714 ACCGAGGCAATGCTAGCTATTGGCAGTAAAGTGCGGCTTACAAACATTAATAAAAAA 773  
 Db 689 ACCGAGGCAATGCTAGCTATTGGCAGTAAAGTGCGGCTTACCTCCCAAAAAAACAG 745  
 Oy 774 AAAAAAAAAAAAAA 788  
 Db 746 TTGTTTCAAGAAA 760  
 RESULT 11  
 AAH5578  
 ID AAH5578 standard; DNA; 404 BP.  
 XX  
 AC AAH5578;  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human breast tumour protein contig 62 DNA sequence.  
 XX  
 KW Cytostatic; vaccine; human; breast-tumour protein; breast cancer;  
 KW gene therapy; de.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200140269-A2.  
 XX  
 PD 07-JUN-2001.  
 PF 29-NOV-2000; 2000WO-US32520.  
 PR 30-NOV-1999; 99US-0451651.  
 PR 22-FEB-2000; 2000US-0510652.  
 PR 10-MAR-2000; 2000US-0523586.  
 PR 07-APR-2000; 2000US-0545068.  
 PR 15-MAY-2000; 2000US-0571025.  
 PA (CORI-) CORIXA CORP.  
 PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;  
 DR MPI; 2001-356154/37.  
 PT Breast tumor polypeptides and the nucleic acids that encode them,  
 PT useful for the prevention, diagnosis and treatment of breast cancer -  
 XX  
 PS Claim 5; Page 154; 221pp; English.  
 XX  
 CC The present sequence is a human breast tumour protein coding sequence.  
 CC This sequence may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the breast tumour  
 CC protein e.g. breast cancer. For example, this sequence may be used to  
 CC treat disorders associated with decreased expression by rectifying  
 CC mutations or deletions in a patient's genome that affect the activity of  
 CC breast tumour protein by expressing inactive proteins or to supplement  
 CC the patients own production of the breast tumour protein. Additionally,

CC the present sequence may be used to produce the breast tumour protein, by  
 CC inserting the nucleic acids into a host cell and culturing the cell to  
 CC express the protein. The present sequence and its complementary sequences  
 CC may also be used as DNA probes in diagnostic assays to detect and  
 CC quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy.

XX Sequence 404 BP; 81 A; 115 C; 109 G; 95 T; 4 other;

Query Match 47.3%; Score 400; DB 22; Length 404;  
 Best Local Similarity 99.0%; Pred. No. 4.4e-64;  
 Matches 400; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 135 ACTGTGAACCTCGGCTTCGAGCGCACTTACTGAGCTGCGCAGTGTGAGAGAGC 194  
 Db 1 ACTGTGAACCTCGGCTTCGAGCGCACTTACTGAGCTGCGCAGTGTGAGAGAGC 60  
 QY 195 AGTATCCGGGCGATGAGATGAGTCGCGGCTCGGGGGGACAGGTGCTTGTGATGAGA 254  
 Db 61 AGTATCCGGGCGATGAGATGAGTCGCGGCTCGGGGGGACAGGTGCTTGTGATGAGA 120  
 QY 255 TAAATGACACGCTGCTTCTCCAGCTGAGAGATGGGGGCTTCCCTATGAGAAAGATC 314  
 Db 121 TAAATGACACGCTGCTTCTCCAGCTGAGAGATGGGGGCTTCCCTATGAGAAAGATC 180  
 QY 315 TCATTGAGGCGCATCCGAGAGCCAGTAATGAGAGAAACCTTGAAGATCACAACAGCC 374  
 Db 181 TCATTGAGGCGCATCCGAGAGCCAGTAATGAGAGAAACCTTGAAGATCACAACAGCC 240  
 QY 375 GTCTCCCTCGCTGATCTCTGTGACTGACACAGACTCTGGGTCTCTGTCTGTGAGGCT 434  
 Db 241 GTCTCCCTCGCTGATCTCTGTGACTGACACAGACTCTGGGTCTCTGTCTGTGAGGCT 300  
 QY 435 CCAACCTTGTCTCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494  
 Db 301 CCAACCTTGTCTCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 495 GCTCTTGAAG 538  
 Db 361 GCTCTTGAAG 404

## RESULT 12

ABV38989 standard; cDNA; 517 BP.

XX ABV38989;

XX 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 38980.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

PN MO200160860-A2.

XX 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PA Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

DR Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer

XX Claim 1; Page 7921; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 517 BP; 118 A; 138 C; 142 G; 119 T; 0 other;

Query Match 45.1%; Score 381.2; DB 23; Length 517;

Best Local Similarity 90.2%; Pred. No. 1.2e-60; Mismatches 23; Indels 25; Gaps 2;

Matches 440; Conservative 0; Mismatches 23; Indels 25; Gaps 2;

QY 139 TGAACCTCGGCGCTTCGAGCGCACTTACTGAGCTGCGCAGTGTGAGAGAGAGAGAG 198  
 Db 30 TGAACCTCGGCGCTTCGAGCGCACTTACTGAGCTGCGCAGTGTGAGAGAGAGAGAG 89  
 QY 199 TCGGGCGATGAGATGAGTCGCGCTCGGGGGACCA----- 235  
 Db 90 TCGGGCGATGAGATGAGTCGCGCTCGGGGGACCA----- 235  
 QY 236 -GGTGCCTTGAATGAGATGAGTAATGAGACAGCTGCTTCCAGCTGAGAGATGGGG 294  
 Db 150 GGTGCCTTGAATGAGATGAGTAATGAGACAGCTGCTTCCAGCTGAGAGATGGGG 209  
 QY 295 CTTTCCCTATGAGAGAGATCTCATTTAGGCGCATCCGAGAGAGAGAGAGAGAGAGAG 354  
 Db 210 CTTTCCCTATGAGAGAGATCTCATTTAGGCGCATCCGAGAGAGAGAGAGAGAGAGAG 269  
 QY 355 AGAAGATACCAACAGCGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413  
 Db 270 AGAAGATACCAACAGCGCGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329  
 QY 414 GTTCCGCTCTGTTCTGGGGGTCGAAACCTTGTCTCTCTTGTGCTGCTGCTGCTGCTGCT 473  
 Db 330 GTTCCGCTCTGTTCTGGGGGTCGAAACCTTGTCTCTCTTGTGCTGCTGCTGCTGCTGCT 389  
 QY 474 CTGCTCTTCTTCT 533  
 Db 390 CTGCTCTTCTTCT 449  
 QY 534 TGGGTACAAAGAGAGATGAGATTCCTGCTTGGGGGCGAGAGAGAGAGAGAGAGAGAG 593  
 Db 450 TGGGTACAAAGAGAGATGAGATTCCTGCTTGGGGGCGAGAGAGAGAGAGAGAGAGAG 509  
 QY 594 ATGAACAC 601  
 Db 510 ATGAACAC 517

## RESULT 13

AA171785 standard; cDNA; 354 BP.

XX AA171785;

```

XX 22-JAN-2002 (first entry)
DT
XX
XX Human C35 coding sequence #1.
DE
XX
XX Human; C35; cytostatic; gene therapy; vaccine; tumour antigen; ss;
KM breast cancer; bladder cancer; tumour immunotherapy; chromosome 17q12.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 7..354
FT /*tag= a
FT /product= "Human C35"
XX
XX WO200174859-A2.
XX
XX 11-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US10855.
XX
XX 04-APR-2000; 2000US-194463P.
XX
XX (UTRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Evans BE, Borrello MA;
XX
XX MPI: 2001-626383/72.
XX
XX P-PSDB; AAG78997.
XX
XX Novel C35 polypeptides and C35 genes useful in immunogenic compositions
PT and vaccines, for inducing antibody and cell-mediated immunity against
PT target cells, such as tumor cells that express C35 gene
XX
XX Claim 1; Fig 1; 331pp; English.
XX
XX The present sequence is human C35 coding sequence. C35 is a novel tumour
CC antigen that is overexpressed in human breast and bladder carcinoma. C35
CC is thought to be a promising candidate for tumour immunotherapy, in
CC immunogenic compositions and vaccines, to induce antibody and
CC cell-mediated immunity against target cells such as tumour cells that
CC express C35 genes. The C35 gene aligns on human chromosome 17q12.
XX
XX Sequence 354 BP; 77 A; 94 C; 120 G; 63 T; 0 other;
XX
XX Query Match 41.9%; Score 354; DB 22; Length 354;
XX Best Local Similarity 100.0%; Pred. No. 1e-55;
XX Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 14
AAH77148
ID AAH77148 standard; cDNA, 354 BP.
XX
XX AAH77148;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX Human C35 gene cDNA sequence.
DE
XX
XX C35; antigenic peptide; major histocompatibility complex; ss;
XX MHC-peptide complex; MHC; human; MHC class I alpha chain; gene;
XX beta-2 microglobulin; MHC class II alpha chain; MHC class II beta chain;
XX vaccine; immune response modulation; hyperproliferative disorder;
XX neoplasm; hypergammaglobulinaemia; viral infection; hepatitis;
XX meningitis; bacterial infection; tuberculosis; gingivitis;
XX parasitic infection; autoimmune disease; Hashimoto's disease;
XX Graves' disease; rheumatoid arthritis; allergy; asthma; organ rejection;
XX graft-versus-host disease; GVHD; breast cancer.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 7..354
FT /*tag= a
FT /partial
FT /product= "C35 protein"
XX
XX WO200178768-A2.
XX
XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US11912.
XX
XX 12-APR-2000; 2000US-196472P.
XX
XX (UTRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX MPI: 2001-602927/68.
XX
XX P-PSDB; AAG77870.
XX
XX Novel compound comprising major histocompatibility complex-peptide
PT complexes, used to modulate immune responses
XX
XX Example 16; Fig 7; 166pp; English.
XX
XX The invention comprises a compound which contains one or more major
CC histocompatibility complex (MHC)-peptide complexes, and an antibody
CC specific for a cell surface marker. The complexes comprise an MHC class
CC I alpha chain, a beta-2 microglobulin molecule and an antigenic peptide
CC bound in the MHC groove. Alternatively, the complexes may comprise an MHC
CC class II alpha chain, an MHC class II beta chain, and an antigenic
CC peptide bound in the MHC groove. The complexes are linked to the carboxyl
CC terminus of the antibody. The compounds of the invention can be used as a
CC vaccine to modulate an immune response. The compounds of the invention
CC are useful for treating: hyperproliferative disorders (e.g. neoplasms and
CC hypergammaglobulinaemia); viral infections (e.g. hepatitis and
CC meningitis); bacterial infections (e.g. tuberculosis and gingivitis) and
CC parasitic infections; autoimmune diseases (e.g. Hashimoto's disease;
CC Graves' disease and rheumatoid arthritis); allergic reactions/conditions
CC (e.g. asthma). The compounds of the invention may also be used in the
CC treatment of organ rejection or graft-versus-host disease (GVHD). The
CC present cDNA sequence represents a gene (C35) that is differentially
CC expressed in human breast cancer cells. In one embodiment of the
CC invention, antigenic peptides derived from C35 protein can be used to
XX promote an immune response against a cancerous cell.
XX
XX Sequence 354 BP; 77 A; 94 C; 120 G; 63 T; 0 other;
XX
XX Query Match 41.9%; Score 354; DB 23; Length 354;

```

Best Local Similarity 100.0%; Pred. No. 1e-55;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 44 GCGCGCATGAGCGGGGAGCGGGGACAGACGTCCTTACGCGCCCTCCCGAGAGGTGAG 103
Db 1 GCGCGCATGAGCGGGGAGCGGGGACAGACGTCCTTACGCGCCCTCCCGAGAGGTGAG 60
QY 104 CCGGCGAGTGGGGTCCGATCGTGTGAGTGAAGTGAACCCGCGGCTTGAAGGCGACC 163
Db 61 CCGGCGAGTGGGGTCCGATCGTGTGAGTGAAGTGAACCCGCGGCTTGAAGGCGACC 120
QY 164 TACCTGAGTGGCGCAGTGTCTGTGAAGAGACAGTATCCGCGCATCGAGTCCGCGC 223
Db 121 TACCTGAGTGGCGCAGTGTCTGTGAAGAGACAGTATCCGCGCATCGAGTCCGCGC 180
QY 224 CTGCGGGGCGACAGTGTCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 283
Db 181 CTGCGGGGCGACAGTGTCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
QY 284 GAGAAATGGGGGCTTCCCTATGAGAAAGATCTCATTTAGAGGCGCATCCGAGAGCAGTAAT 343
Db 241 GAGAAATGGGGGCTTCCCTATGAGAAAGATCTCATTTAGAGGCGCATCCGAGAGCAGTAAT 300
QY 344 GAGAAATCCCTAGAAAGATCACCACAGCGCTCTCCCTGCGTCACTCTGTGA 397
Db 301 GAGAAATCCCTAGAAAGATCACCACAGCGCTCTCCCTGCGTCACTCTGTGA 354
```

RESULT 15  
ABV96744  
ID ABV96744 standard; cDNA; 346 BP.

XX AC ABV96744;

DT 14-JAN-2003 (first entry)

XX DE Human pancreatic cancer expressed cDNA SEQ ID NO 2152.

XX DE Human pancreatic cancer; gene therapy; vaccine; immunostimulant;

XX KM Cytostratic; tumour; gene; ss.

XX OS Homo sapiens.

XX PN WO200260317-A2.

XX PD 08-AUG-2002.

XX PF 30-JAN-2002; 2002WO-US02781.

XX PR 30-JAN-2001; 2001US-265305P.

XX PR 31-JAN-2001; 2001US-265682P.

XX PR 09-FEB-2001; 2001US-267568P.

XX PR 21-MAR-2001; 2001US-278651P.

XX PR 28-APR-2001; 2001US-287112P.

XX PR 16-MAY-2001; 2001US-291631P.

XX PR 12-JUL-2001; 2001US-305484P.

XX PR 20-AUG-2001; 2001US-313999P.

XX PR 27-NOV-2001; 2001US-333626P.

XX PA (CORI-) CORIXA CORP.

XX PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX DR WPI; 2002-627435/67.

XX PT New isolated polynucleotide and pancreatic tumor polypeptides, useful  
XX PT for diagnosing, preventing and/or treating cancer, particularly  
XX PT pancreatic cancer  
XX PS Claim 1, SEQ ID NO 2152; 300bp + Sequence Listing; English.  
XX CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
XX CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);

CC (b) complements of (a); (c) sequences consisting of at least 20  
CC contiguous residues of (a); (d) sequences that hybridize to (a), under  
CC moderately stringent conditions; (e) sequences having at least 75% or 90%  
CC identity to (a); or (f) degenerate variants of (a). Polypeptides  
CC (ABP8596-ABP8637) encoded by (I) and oligonucleotide can be used to  
CC detect cancer in a patient and compositions comprising polypeptides and  
CC polynucleotides, antibodies, fusion proteins, T cell populations and  
CC antigen presenting cells expressing the polypeptide are useful in  
CC treating pancreatic cancer and stimulating an immune response. The  
CC polynucleotides can be used as probes or primers for nucleic acid  
CC hybridization, in the design and preparation of ribozyme molecules for  
CC inhibiting expression of the tumour polypeptides and proteins in the  
CC tumour cells, in vaccines and for gene therapy.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 346 BP; 70 A; 101 C; 91 G; 84 T; 0 other;

Query Match 40.9%; Score 346; DB 24; Length 346;

Best Local Similarity 100.0%; Pred. No. 3e-54;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 193 GCAGTATCCGGGCGATGAGATGAGTCCGCGCTCGGGGCGACAGTGCCTTTGAGATAGA 252
Db 1 GCAGTATCCGGGCGATGAGATGAGTCCGCGCTCGGGGCGACAGTGCCTTTGAGATAGA 60
QY 253 GATTAATGACACAGCTGTGTCTCCCAAGCTGAGTAATGGGGGGCTTCCCATGAGAAAGA 312
Db 61 GATTAATGACACAGCTGTGTCTCCCAAGCTGAGTAATGGGGGGCTTCCCATGAGAAAGA 120
QY 313 TCTCATTTGAGGCGCATCCGAAAGCCAGTAATGAGAAACCTTGAAGATCAACCAAG 372
Db 121 TCTCATTTGAGGCGCATCCGAAAGCCAGTAATGAGAAACCTTGAAGATCAACCAAG 180
QY 373 CCGTCTCTCCCTGCGTATCTGTGACTGACACAGGATCTTGGGTTCTCTGTTCTGGG 432
Db 181 CCGTCTCTCCCTGCGTATCTGTGACTGACACAGGATCTTGGGTTCTCTGTTCTGGG 240
QY 433 GTCCAAACCTTGGTCCCTTGGTGTCTGCTGGGAGCTCCCGCTGCTTTCCCTACT 492
Db 241 GTCCAAACCTTGGTGTCTGCTGGTGTCTGCTGGGAGCTCCCGCTGCTTTCCCTACT 300
QY 493 TAGCTCTTAGCAAGAGACCTGCGCTCCACTTTGCCCTTTGGGT 538
Db 301 TAGCTCTTAGCAAGAGACCTGCGCTCCACTTTGCCCTTTGGGT 346
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Search completed: December 18, 2003, 20:48:59  
Job time : 304 secs



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Query Match          9.8%; Score 82.4; DB 4; Length 588;
Best Local Similarity 91.6%; Pred. No. 1.5e-09;
Matches 87; Conservative 0; Mismatches 8; Indels 0; Gaps 0

QY 751 CTACAAACACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 552

QY 811 AAAAAAAAAAATNTMTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 845
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 AAAAAAAAAAAAAAAAANNCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 587

RESULT 2
US-09-370-807-7
; Sequence 7; Application US/09370807
; Patent No. 6297034

```

[illegible][illegible]





OY	686	GCGCCAGATTATTTATTTCTCCCTAACCGGGCAATGCAGTATGTGCGACGTAAAG	745
Db	1211	TGCTTCAGTGTGAATATTAATTTGAAACTCATGAGATATAAACCCTTATATTATTAT	1270
OY	746	TGGCGCTACAACACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	805
Db	1271	TATATAA	1331
OY	806	AAAAAAAAAAAAAAAAATNTNGGGGGG	832
Db	1331	AAAAAAAAAAAAAAAAAAGGGCGG	1357

```

10 RESULT 10
20 US-09-461-325-44
30 Sequence 44, Application US/09461325A
40 Patent No. 6475753
50 GENERAL INFORMATION:
60 APPLICANT: Ruben et al.
70 TITLE OF INVENTION: 94 Human Secreted Proteins
80 FILE REFERENCE: P20029P1
90 CURRENT APPLICATION NUMBER: US/09/461.325A
100 CURRENT FILING DATE: 1999-12-14
110 EARLIER APPLICATION NUMBER: PCT/US99/13418
120 EARLIER FILING DATE: 1999-06-15
130 EARLIER APPLICATION NUMBER: 60/089,507
140 EARLIER FILING DATE: 1998-06-16
150 EARLIER APPLICATION NUMBER: 60/089,508
160 EARLIER FILING DATE: 1998-06-16
170 EARLIER APPLICATION NUMBER: 60/089,509
180 EARLIER FILING DATE: 1998-06-16
190 EARLIER APPLICATION NUMBER: 60/089,510
200 EARLIER FILING DATE: 1998-06-16
210 EARLIER APPLICATION NUMBER: 60/090,112
220 EARLIER FILING DATE: 1998-06-22
230 EARLIER APPLICATION NUMBER: 60/090,113
240 EARLIER FILING DATE: 1998-06-22
250 NUMBER OF SEQ ID NOS: 532
260 SOFTWARE: PatentIn Ver. 2.0
270 SEQ ID NO 44
280 LENGTH: 569
290 TYPE: DNA
300 ORGANISM: Homo sapiens
310 US-09-461-325-44

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```
Query Match      8.3%; Score 70.2; DB 4; Length 569;
Best local Similarity 88.2%; Pred No. 7.2e-07;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0

OY       753 ACACAACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 812
          ||| |
Db        485 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 544
                ||| |
OY       813 AAAAAAAAAATNTNGGGGGGCGGCC 837
          |||||
Db        545 AAAAAAAAAAAAAAAAAAGGGGGGCCCC 569

RESULT 11
US-09-404-879A-261/c
; Sequence 261, Application US/09404879A
; Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon B.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                    DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FaSTSeq For Windows Version 3.0
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; SEQ ID NO 261
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-261
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Query Match	8.3%	Score 70;	DB 4;	Length 94;
Best Local Similarity	91.2%	Pred. No. 4.7e-07;		
Matches 73; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Oy	762	AAA	821
Dd	93	AAA	34
Oy	822	TNTNNGGGGGGCCCCCCC	841
Dd	33	AAAAAAAAAGGAACCTGCCC	14

```

RESULT 12
US-09-338-933-261/c
; Sequence 261, Application US/09338933
; Patent No. 6489831
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462CJ
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-261

```

	8.3%	Score	70;	DB	4;	Length	94;		
Query Match	Best Local Similarity	91.2%	Pred.	No.	4.7e-07;	Mismatches	7;		
	Matches	73;	Conservative	0;	Mismatches	7;	Indels	0;	
								Gaps	0;
OY	762	AAA							821
Dd	93	AAA							34
OY	822	TNTNGGGGGGGCCCCC							841
Dd	33	AAAAGGGGGGACCTGCC							14

```

RESULT 13-
US-09-215-681-261/c
; Sequence 261, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 261
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-215-681-261

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RESULT 15  
US-09-152-060-15  
Sequence 15, Application US/09152060  
Patent No. 6448230  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 28 Human Secreted Proteins  
FILE REFERENCE: P2003PL.US  
CURRENT APPLICATION NUMBER: US/09/152.060

Search completed: December 18, 2003, 22:37:42  
Job time : 74 secs



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Db      61 GCGGGGAGAGCGTCCGAGGCGCCCTCCCGAGAGGTGAGCGGAGGTGCGG 120
Qy      121 CATGTGTGTGAGTCTGTGAACCTCTGGGTGAGGCGCACTTCTGAGCTGGCCAG 180
Db      121 CATGTGTGTGAGTCTGTGAACCTCTGGGTGAGGCGCACTTCTGAGCTGGCCAG 180
Qy      181 TGCTGTGAAGAGATCCGGGCGATCGAGATGAGTCGGGCGCTCGGGGGCAGAGTGC 240
Db      181 TGCTGTGAAGAGATCCGGGCGATCGAGATGAGTCGGGCGCTCGGGGGCAGAGTGC 240
Qy      241 CTTTGAGATGAGATTAATGAGACAGTGTGTCTTCCAGCTGAGAAATGGGGCTTTC 300
Db      241 CTTTGAGATGAGATTAATGAGACAGTGTGTCTTCCAGCTGAGAAATGGGGCTTTC 300
Qy      301 CTATGAGAAAGATCTCTTGAAGGCGATCCGAGAGCCAGTAATGAGAAACCTTGA 360
Db      301 CTATGAGAAAGATCTCTTGAAGGCGATCCGAGAGCCAGTAATGAGAAACCTTGA 360
Qy      361 GATCACAAGAGCGCTCTCCCTGCTCATCTGTGACTGACAGAGACTCTGGGTTCTG 420
Db      361 GATCACAAGAGCGCTCTCCCTGCTCATCTGTGACTGACAGAGACTCTGGGTTCTG 420
Qy      421 CTCTGTTCTGGGGTCCAAACCTTGGTCTCTCTGCTGAGAGCTTCCCTGCT 480
Db      421 CTCTGTTCTGGGGTCCAAACCTTGGTCTCTCTGCTGAGAGCTTCCCTGCT 480
Qy      481 CTTTCCCTCTACTTGAAGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      481 CTTTCCCTCTACTTGAAGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy      541 AAGAGAGAGATTAAGAGATCCGTGGGCTTGGGGGCGAGAGAGAGAGAGAGAGAG 600
Db      541 AAGAGAGAGATTAAGAGATCCGTGGGCTTGGGGGCGAGAGAGAGAGAGAGAGAG 600
Qy      601 CTTTCCAGGCACTCATACCCCTTCCAGGTAAGTCCAGAGAGAGAGAGAGAGAG 660
Db      601 CTTTCCAGGCACTCATACCCCTTCCAGGTAAGTCCAGAGAGAGAGAGAGAGAG 660
Qy      661 CTTGCGCTCGTATATCTGTCTGATGCGACAGATTTTATTTATTTCCCTTA 720
Db      661 CTTGCGCTCGTATATCTGTCTGATGCGACAGATTTTATTTATTTCCCTTA 720
Qy      721 GCAATGCTAGCTATTTGGCAGTAAGTGGCGCTACAAACATAAATAAATAAATAA 780
Db      721 GCAATGCTAGCTATTTGGCAGTAAGTGGCGCTACAAACATAAATAAATAAATAA 780
Qy      781 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 840
Db      781 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 840
Qy      841 CCCCC 845
Db      841 CCCCC 845

```

## RESULT 2

```

US-10-177-293-479
; Sequence 479, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Gialt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangl
; APPLICANT: Mertens, Maureen
; APPLICANT: Meyer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.

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; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzos, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Miller, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-479

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Query Match      89.7%; Score 758; DB 15; Length 1057;
Best Local Similarity 99.9%; Pred. No. 1,1e-159;
Matches 763; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      10 TCACACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 69
Db      289 TCACACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 347
Qy      70 GAGTCGCTGAGGCGCCCTTCCGAGAGAGTGAAGCGGAGAGAGAGAGAGAGAGAG 129
Db      348 GAGTCGCTGAGGCGCCCTTCCGAGAGAGTGAAGCGGAGAGAGAGAGAGAGAGAG 407
Qy      130 GGAATCTGTGAACCTCGGAGCTTTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 189
Db      408 GGAATCTGTGAACCTCGGAGCTTTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 467
Qy      190 GAGCAGATATCCGGGAGTGAAGTGAAGTGCCTTCGGGGGAGAGAGAGAGAGAG 249
Db      468 GAGCAGATATCCGGGAGTGAAGTGAAGTGCCTTCGGGGGAGAGAGAGAGAGAG 527
Qy      250 AGAGATTAATGAGACAGCTGTGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309
Db      528 AGAGATTAATGAGACAGCTGTGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 587
Qy      310 AGATCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369
Db      588 AGATCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
Qy      370 CAGCGCTCTCTCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 429
Db      648 CAGCGCTCTCTCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 707
Qy      430 GGGGTCAAACTTGTGTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489
Db      708 GGGGTCAAACTTGTGTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 767
Qy      490 ACTTAGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549
Db      768 ACTTAGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827
Qy      550 ATGAGAGATTCGTTGGGCTTTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609

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Db 828 ATAGAAGATTCGGTGGCCCTTGGGGGAGAGAGACCTCTCATGAACACTCTCTCAG 887  
QY 610 CCACCTCATACCCCTTCCTCCAGGTAAGTGGCCAGAAAGCCAGTCCACTCTGGCCCTC 669  
Db 888 CCACTCTATCCCTCTTCCAGGGTAAGTGGCCAGAAAGCCAGTCCACTCTGGCCCTC 947  
QY 670 GGTAAATACCTGTCTGATGCGACAGATTTTATTTATTTCTCCCTAAACCAGGCAATGTCA 729  
Db 948 GGTAAATACCTGTCTGATGCGACAGATTTTATTTATTTCTCCCTAAACCAGGCAATGTCA 1007  
QY 730 GCTATTGGCAGTAAGTGGCGCTTACAAACACTTAAAAA 779  
Db 1008 GCTATTGGCAGTAAGTGGCGCTTACAAACACTTAAAAA 1057

RESULT 3  
US-09-824-787B-5  
; Sequence 5, Application US/09824787B  
; Patent No. US20020155447A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Evans, Elizabeth E.  
; APPLICANT: Borrello, Melinda A.  
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and  
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides  
; FILE REFERENCE: 1821.0040001  
; CURRENT APPLICATION NUMBER: US/09/824,787B  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,463  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (608)..(608)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
US-09-824-787B-5

Query Match 80.3%; Score 678.8; DB 10; Length 683;  
Best Local Similarity 99.6%; Pred. No. 4,7e-142;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 59 GAGCGGGGAGAGCGTCCGTAGCGCCCTCCGAGAGGTGAGCCGGGAGTGG36TTC 118  
Db 1 GAGCGGGGAGAGCGTCCGTAGCGCCCTCCGAGAGGTGAGCCGGGAGTGG36TTC 60  
QY 119 GCGATCGTGTGAGTATCTGTGAACCCCTGCGGCTTCGAGCGCACTTACCTGAGT36CC 178  
Db 61 GCGATCGTGTGAGTATCTGTGAACCCCTGCGGCTTCGAGCGCACTTACCTGAGT36CC 120  
QY 179 AGTGTGTGAAGAGCAGTATCCGGGCAATCGAGTCAGTCCGCGCTCGGGGGCAGAGT 238  
Db 121 AGTGTGTGAAGAGCAGTATCCGGGCAATCGAGTCAGTCCGCGCTCGGGGGCAGAGT 180  
QY 239 GCTTTGAGATAGATTAATGAGCAGCTGTGTCTTCCAAAGCTGAGAAATGGGGCTTT 298  
Db 181 GCTTTGAGATAGATTAATGAGCAGCTGTGTCTTCCAAAGCTGAGAAATGGGGCTTT 240  
QY 299 CCGTATGAGAAAGATCTCATTTAGAGCCATCCGAAAGCCAGTAATGAGAAACCTTAAGA 358  
Db 241 CCGTATGAGAAAGATCTCATTTAGAGCCATCCGAAAGCCAGTAATGAGAAACCTTAAGA 300  
QY 359 AAGATCAACAACAGCGTCTCCCTGCGTCACTGTGATGCAAGAGACTGTGGGTTCC 418  
Db 301 AAGATCAACAACAGCGTCTCCCTGCGTCACTGTGATGCAAGAGACTGTGGGTTCC 360  
QY 419 TGCTCTGTTCTTGGGGTCCAAACCTTTGTTCTCTTTGGTCTGTTGGAGTCTCCCTGTC 478  
Db 361 TGCTCTGTTCTTGGGGTCCAAACCTTTGTTCTCTTTGGTCTGTTGGAGTCTCCCTGTC 420

QY 479 CTCTTCCCTACTAGTCTCTTACCAAGAGACCCCTGGCTCCACTTTGGCCTTTGGGT 538  
Db 421 CTCTTCCCTACTAGTCTCTTACCAAGAGACCCCTGGCTCCACTTTGGCCTTTGGGT 480  
QY 539 ACAAGAAAGATAGAAATTCCTGCGCTTGGGGGAGAGAGACACTCTTCATGAA 598  
Db 481 ACAAGAAAGATAGAAATTCCTGCGCTTGGGGGAGAGAGACACTCTTCATGAA 540  
QY 599 CACTTTCACACCACTCATACCCCTTCCAGGGTAAGTGGCCAGAAACCCAGTCCA 658  
Db 541 CACTTTCACACCACTCATACCCCTTCCAGGGTAAGTGGCCAGAAACCCAGTCCA 600  
QY 659 CTCTTCCCTGCTGATATCTGTGATGCGACAGATTTTATTTATTTCTCCCTTAACCA 718  
Db 601 CTCTTCCCTGCTGATATCTGTGATGCGACAGATTTTATTTATTTCTCCCTTAACCA 660  
QY 719 GGGCAATGTAGCTATTGGCAGT 741  
Db 661 GGGCAATGTAGCTATTGGCAGT 683

RESULT 4  
US-09-824-787B-19  
; Sequence 19, Application US/09824787B  
; Patent No. US20020155447A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Evans, Elizabeth E.  
; APPLICANT: Borrello, Melinda A.  
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and  
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides  
; FILE REFERENCE: 1821.0040001  
; CURRENT APPLICATION NUMBER: US/09/824,787B  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,463  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
US-09-824-787B-19

Query Match 68.2%; Score 576; DB 10; Length 584;  
Best Local Similarity 100.0%; Pred. No. 4.1e-119;  
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 GCGGGAGCCCGGGGAGAGCGTCCGTAGCGCCCTCCGAGAGGTGAGCCGGGAGTGG 113  
Db 9 GCGGGAGCCCGGGGAGAGCGTCCGTAGCGCCCTCCGAGAGGTGAGCCGGGAGTGG 68  
QY 114 GGGTCCGATCGTGTGAGTATCTGTGAACCTTCGGGCTTCGAGGCGAATCTGAGC 173  
Db 69 GGGTCCGATCGTGTGAGTATCTGTGAACCTTCGGGCTTCGAGGCGAATCTGAGC 128  
QY 174 TGGCGAGCTGTGAAGAGAGATCCGGGCAATCGAGTCAGTCCGCGCTCGGGGGCA 233  
Db 129 TGGCGAGCTGTGAAGAGAGATCCGGGCAATCGAGTCAGTCCGCGCTCGGGGGCA 188  
QY 234 CAGTGTCTTGAATAGATTAATGAGCAGCTGTGTCTTCCAAAGCTGAGAAATGGGG 293  
Db 189 CAGTGTCTTGAATAGATTAATGAGCAGCTGTGTCTTCCAAAGCTGAGAAATGGGG 248  
QY 294 GCTTTCCTTGAAGAAAGATCTCATTTAGAGCCATCCGAAAGCCAGTAATGAGAAACC 353  
Db 249 GCTTTCCTTGAAGAAAGATCTCATTTAGAGCCATCCGAAAGCCAGTAATGAGAAACC 308

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QY 354 TAGAAAAATACCAACAGCGCTGCTCCCTGCGTCATCTGTGATGTCACAGAGACTCTGG 413
Db 309 TAGAAAAATACCAACAGCGCTGCTCCCTGCGTCATCTGTGATGTCACAGAGACTCTGG 368
QY 414 GTTCTGCTGCTGTTCTGGGGGTCCAAACCTTGGTCTCCCTTTGGTCTGCTGGAGCTCCC 473
Db 369 GTTCTGCTGCTGTTCTGGGGGTCCAAACCTTGGTCTCCCTTTGGTCTGCTGGAGCTCCC 428
QY 474 CTTGCTCTTTCCCTCTAATTAGCTCTCTTACCAAGAAACCTGGCCCTCCACTTTGCCCTT 533
Db 429 CTTGCTCTTTCCCTCTAATTAGCTCTCTTACCAAGAAACCTGGCCCTCCACTTTGCCCTT 488
QY 534 TGGGTACAAAGAAAGATAGAAATTCCTGGCTTGGGGGACAGAGAGACACTCTCC 593
Db 489 TGGGTACAAAGAAAGATAGAAATTCCTGGCTTGGGGGACAGAGAGACACTCTCC 548
QY 594 ATGAACACTTCTCCAGCCACTCTACCCCTTCCC 629
Db 549 ATGAACACTTCTCCAGCCACTCTACCCCTTCCC 584

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RESULT 5
US-09-824-787B-33/c
; Sequence 33, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-787B-33

```

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Query Match 63.0%; Score 532; DB 10; Length 532;
Best Local Similarity 100.0%; Pred. NO. 2.7e-109; Mismatches 0; Indels 0; Gaps 0;
Matches 532; Conservative 0;

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QY 233 ACAAGTCCCTTGAATAGATATAATGACAGCTGCTGTTCTCCAGCTGAGATGAG 292
Db 532 ACAAGTCCCTTGAATAGATATAATGACAGCTGCTGTTCTCCAGCTGAGATGAG 473
QY 293 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 352
Db 472 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 413
QY 472 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 412
Db 412 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 353
QY 412 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 412
Db 412 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 353
QY 413 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 472
Db 352 GGGTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCAGTATGAGAAACC 293
QY 473 CCGTCCCTCTTCCCTAATAGCTCTTACCAAGAGACCTGGCTCCACTTTGCCCT 532
Db 292 CCGTCCCTCTTCCCTAATAGCTCTTACCAAGAGACCTGGCTCCACTTTGCCCT 233
QY 533 TTGGGTACAAAGAAAGATAGAAATTCCTGGCTTGGGGGACAGAGAGACACTCTC 592
Db 232 TTGGGTACAAAGAAAGATAGAAATTCCTGGCTTGGGGGACAGAGAGACACTCTC 173
QY 593 CATGAACACTTCTCAGGACCTCATACCCCTTCCAGGGTAAGTGCACAGAAAGCC 652

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Db 172 CATGAACACTTCTCAGGACCTCATACCCCTTCCAGGGTAAGTGCACAGAAAGCC 113
QY 653 AGTCCACTCTTGGCCCTCGGTAATACCTGTCTGATGTCACAGATTTATTTATTCCTCCCT 712
Db 112 AGTCCACTCTTGGCCCTCGGTAATACCTGTCTGATGTCACAGATTTATTTATTCCTCCCT 53
QY 713 AACCCAGGCAATGTGAGCTATTTGAGCAATTAAGTGGCGCTACAAACACTAAA 764
Db 52 AACCCAGGCAATGTGAGCTATTTGAGCAATTAAGTGGCGCTACAAACACTAAA 1

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RESULT 6
US-09-824-787B-35/c
; Sequence 35, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (393)..(393)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c
; NAME/KEY: misc_feature
; LOCATION: (482)..(482)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c
; NAME/KEY: misc_feature
; LOCATION: (503)..(503)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c
; NAME/KEY: misc_feature
; LOCATION: (520)..(520)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c
US-09-824-787B-35

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Query Match 61.0%; Score 515.8; DB 10; Length 571;
Best Local Similarity 95.8%; Pred. NO. 1.1e-105;
Matches 549; Conservative 0; Mismatches 21; Indels 3; Gaps 2;

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QY 190 GAGACGATATCCGGGCAATGAGATCGAGTCGGCCCTCGGGGGACAGGTGCCCTTGAGAT 249
Db 571 GAGACGATATCCGGGCAATGAGATCGAGTCGGCCCTCGGGGGACAGGTGCCCTTGAGAT 512
QY 250 AGAGATTAATGAGACAGCTGCTGTTCTCAAGCTGAGAAATGGGGGCTTTCCCTATGAGAA 309
Db 511 AGAGATTAATGAGACAGCTGCTGTTCTCAAGCTGAGAAATGGGGGCTTTCCCTATGAGAA 454
QY 310 AGATTCATTTAGAGGCAATCGAAGACAGTAATGAGAAACCTTGAAGAAATGATCAACAA 369
Db 453 AGATTCATTTAGAGGCAATCGAAGACAGTAATGAGAAACCTTGAAGAAATGATCAACAA 394
QY 370 CAGCGCTCTCTCTGGCTCATCTGTGACTGACAGAGACTTGGGTTCTGCTGCTGTTCT 429
Db 393 CAGCGCTCTCTCTGGCTCATCTGTGACTGACAGAGACTTGGGTTCTGCTGCTGTTCT 334
QY 430 GGGGTCAAAACCTTGGATCTCCCTTTGGCTGCTGGAGAGCTCCCGTCCCTTTCCCT 489
Db 333 GGGGTCAAAACCTTGGATCTCCCTTTGGCTGCTGGAGAGCTCCCGTCCCTTTCCCT 274
QY 490 ACTTAGCTCTTGAAGAAAGACCTGGGCTCCACTTTGGCTTGGGTACAAAGAGGA 549

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Db 273 ACTTGGCTCTTAGCAAAAGAGACCTGGCTCCTCCTTGGTGGTAACAAGAGA 214  
Qy 550 ATAGAGATTCCGTGGCCCTTGGGGGAGAGAGACACTCCCAATGAAACATTTCCAG 609  
Db 213 ATAGAGATTCCGTGGCCCTTGGGGGAGAGAGACACTCCCAATGAAACATTTCCAG 154  
Qy 610 CC-ACCTCATACCCCTTCCAGGGTAATGCGCAAGAAAGCCAGTCCTTTCGCT 668  
Db 153 CCACTCATACCCCTTCCAGGGTAATGCGCAAGAAAGCCAGTCCTTTCGCT 94  
Qy 669 CCGTAATACCTGTCTGATGCCACAGATTTTATTTATTTCTCCCTAACCCAGGCAATGTC 728  
Db 93 CCGTAATACCTGTCTGATGCCACAGATTTTATTTATTTCTCCCTAACCCAGGCAATGTC 34  
Qy 729 AGCTATGGCAGTAAGTGCGGCTACAAACACT 761  
Db 33 AGCTATGGCAGTAAGTGCGGCTACAAACACT 1

RESULT 7  
US-09-824-787B-37/C

; Sequence 37, Application US/09824787B  
; Patent No. US2002015547A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Evans, Elizabeth E.  
; APPLICANT: Borrello, Melinda A.  
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and  
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides  
; FILE REFERENCE: 1821.0040001  
; CURRENT APPLICATION NUMBER: US/09/824,787B  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,463  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
; NAME/KEY: misc\_feature  
; LOCATION: (299)..(299)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
; NAME/KEY: misc\_feature  
; LOCATION: (387)..(387)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
; NAME/KEY: misc\_feature  
; LOCATION: (520)..(520)  
; OTHER INFORMATION: n is any nucleotide of a, t, g or c  
US-09-824-787B-37

Query Match 50.1%; Score 507.8; DB 10; Length 528;

Best Local Similarity 98.9%; Pred. No. 6.8e-104; Mismatches 5; Indels 1; Gaps 1;

Matches 520; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
Qy 242 TTTGAGATAGATTAATGACAGCTGGTGTCTCCAGCTGAGAAATGGGGGCTTTCC 301  
Db 527 TTTGAGAGAGATTAATGACAGCTGGTGTCTCCAGCTGAGAAATGGGGGCTTTCC 468  
Qy 302 TATGAGAAAGATCTCATTTGAGGCGCATCCGAAGAGCCAGTAATGAGAAACCTTAGAAG 361  
Db 467 TATGAGAAAGATCTCATTTGAGGCGCATCCGAAGAGCCAGTAATGAGAAACCTTAGAAG 408  
Qy 362 ATCAACAACGCCGCTCCCTGCTCATCTGTATCTGCAC-AGAGCTTGGGTTCTG 420  
Db 407 ATCAACAACGCCGCTCCCTGCTCATCTGTATCTGCAC-AGAGCTTGGGTTCTG 348  
Qy 421 CTCGTCTGGGGTCAAAACCTTGGTCTCCCTTGGTCTGCTGGAGCTCCCTCTGCT 480

Db 347 CTCGTCTGGGGTCAAAACCTTGGTCTCCCTTGGTCTGCTGGAGMTCCCTGCT 288  
Qy 481 CTTTCCCTACTTACTGCTCTTATGCAAGAGACCTTGCTTCACTTTGCTTGGGTAC 540  
Db 287 CTTTCCCTACTTACTGCTCTTATGCAAGAGACCTTGCTTCACTTTGCTTGGGTAC 228  
Qy 541 AAAGAGAAATAGAAAGATTCGTGGCCCTTGGGGGAGAGAGACACTTCCATGAA 600  
Db 227 AAAGAGAAATAGAAAGATTCGTGGCCCTTGGGGGAGAGAGACACTTCCATGAA 168  
Qy 601 CTTTCCAGCCACTCATACCCCTTCCAGGGTAATGCGCAAGAAAGCCAGTCCT 660  
Db 167 CTTTCCAGCCACTCATACCCCTTCCAGGGTAATGCGCAAGAAAGCCAGTCCT 108  
Qy 661 CTTGCGCTCGGTATATCTGTCTGATGCGCACAGATTTTATTTATTTCTCCCTAACCCAGG 720  
Db 107 CTTGCGCTCGGTATATCTGTCTGATGCGCACAGATTTTATTTATTTCTCCCTAACCCAGG 48  
Qy 721 GCAATGTCAGCTATTGGCAGTAAGTGCGGCTACAAACACTTAA 766  
Db 47 GCAATGTCAGCTATTGGCAGTAAGTGCGGCTACAAACACTTAA 2

RESULT 8  
US-09-824-787B-65/C

; Sequence 65, Application US/09824787B  
; Patent No. US2002015547A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Evans, Elizabeth E.  
; APPLICANT: Borrello, Melinda A.  
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and  
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides  
; FILE REFERENCE: 1821.0040001  
; CURRENT APPLICATION NUMBER: US/09/824,787B  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/194,463  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-824-787B-65

Query Match 58.9%; Score 497.8; DB 10; Length 501;  
Best Local Similarity 99.6%; Pred. No. 1.1e-101; Mismatches 2; Indels 0; Gaps 0;

Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 263 CAGCTGTGTCTTCCAGCTGAGAAATGGGGGCTTTCCATATGAGAAATCTGATGAG 322  
Db 501 CAGCTGTGTCTTCCAGCTGAGAAATGGGGGCTTTCCATATGAGAAATCTGATGAG 442  
Qy 323 GGCATCCGAAGAGCACTAATGAGAAACCTTAGAAGATCAAGCAACCCGCTCC 382  
Db 441 GGCATCCGAAGAGCACTAATGAGAAACCTTAGAAGATCAAGCAACCCGCTCC 382  
Qy 383 TGCCTCATCTGTATGACACAGACTCTGGGTTCTGCTGTCTTGGGGTCCAAACT 442  
Db 381 TGCCTCATCTGTATGACACAGACTCTGGGTTCTGCTGTCTTGGGGTCCAAACT 322  
Qy 443 TGTCTCTCTTGTCTGTCTGGAGCTCCCTGCTCTTCTCTTCTTACTTACTCTTA 502  
Db 321 TGTCTCTCTTGTCTGTCTGGAGCTCCCTGCTCTTCTCTTCTTACTTACTCTTA 262  
Qy 503 GCAAGAGACCTCGGCTTCCACTTTGGCTTGGGTACAAAGAAATAGAAATTCG 562  
Db 261 GCAAGAGACCTCGGCTTCCACTTTGGCTTGGGTACAAAGAAATAGAAATTCG 202  
Qy 563 TGGCTTGGGGGAGAGAGACACTCTCATGAAACATTTCCAGCCACTCATACC 622

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Db      201 TGGCCTTGGGGGAGAGAGACACTCTCCATGACCTTCTCAGCACCCTCATACC 142
Qy      623 CCTTCCAGGGTAGTGTCCCAAGAGCCAGTCTCTTGGCTGGTAATACCTGTC 682
Db      141 CTTCCAGGGTAGTGTCCCAAGAGCCAGTCTCTTGGCTGGTAATACCTGTC 82
Qy      683 TGAATGCACAGATTTTATTTATTTCTCCCTTACCAGGAGCAATGTACGATTGGCAGTA 742
Db      81 TGAATGCACAGATTTTATTTATTTCTCCCTTACCAGGAGCAATGTACGATTGGCAGTA 22
Qy      743 AAGTGGCGCTACAAACACTAA 763
Db      21 AAGTGGCGCTACAAACACTAA 1

RESULT 9
US-09-824-787B-3
; Sequence 3, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-787B-3

Query Match      56.6%; Score 478.2; DB 10; Length 518;
Best Local Similarity 98.6%; Pred. No. 2.8e-97;
Matches 503; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy      54 GCGGGAGAGCCGGGAGAGAGTCCGTAAGGCCCTCCCGAGAGAGTGAAGCCGGGCAATG 113
Db      11 GAGGCTAGCCGGGAGAGAGTCCGTAAGGCCCTCCCGAGAGAGTGAAGCCGGGCAATG 70
Qy      114 GGGTCCGATCGTGTGAGTGAATCCCTCGGCTTGAAGGCGAATCTGAGAGC 173
Db      71 GGGTCCGATCGTGTGAGTGAATCCCTCGGCTTGAAGGCGAATCTGAGAGC 130
Qy      174 TGGCAGTGTGTAAGAGAGATCCGGGATCGAGTGAATCGGAGCTCGGGGCA 233
Db      131 TGGCAGTGTGTAAGAGAGATCCGGGATCGAGTGAATCGGAGCTCGGGGCA 190
Qy      234 CAGGTGCTTGAATAGATTAATGAGACAGTGTGTTTCCAAAGCTGAGATGGGG 293
Db      191 CAGGTG-CTTGAATAGATTAATGAGACAGTGTGTTTCCAAAGCTGAGATGGGG 249
Qy      294 GCTTCCCTATGAGAAAGATTCATTGAGGCCATCCGAGAGCAATGAGAAACC 353
Db      250 GCTTCCCTATGAGAAAGATTCATTGAGGCCATCCGAGAGCAATGAGAAACC 309
Qy      354 TAGAAAGATCAACAAGCGGCTCTCGCTGATCTGTGACTGACAGAGACTGG 413
Db      310 TAGAAAGATCAACAAGCGGCTCTCGCTGATCTGTGACTGACAGAGACTGG 369
Qy      414 GTTCTGCTCTGTCTGGGGTCAAAACCTGTGCTCTTGTGCTGTGAGAGTCCC 473
Db      370 GTTCTGCTCTGTCTGGGGTCAAAACCTGTGCTCTTGTGCTGTGAGAGT-CC 428
Qy      474 CTGCTCTCTTCCCTACTTAAGTCTCTTAAGAAAGAGACCTGGGCTTCACTTGGCCTT 533
Db      429 CTGCTCTCTTCCCTACTTAAGTCTCTTAAGAAAGAGACCTGGGCTTCACTTGGCCTT 488

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Qy      534 TGGGTACAAAGAGATTAAGATTCCGT 563
Db      489 TGGGTACAAAGAGATTAAGATTCCGT 518

RESULT 10
US-09-824-787B-20
; Sequence 20, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-787B-20

Query Match      56.2%; Score 474.8; DB 10; Length 488;
Best Local Similarity 99.6%; Pred. No. 1.6e-96;
Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      35 GCGGACCCGGCGGATGAGCGGGGAGCCGGGAGAGTCCGTAAGGCCCTCCCGAG 94
Db      11 GCGGAGCCGGCGGATGAGCGGGGAGCCGGGAGAGTCCGTAAGGCCCTCCCGAG 70
Qy      95 GAGGTGAGCCGGGAGTGGGATCCGATCTGTGAGTGAATCCCTGCGCTTC 154
Db      71 GAGGTGAGCCGGGAGTGGGATCCGATCTGTGAGTGAATCCCTGCGCTTC 130
Qy      155 GAGGCGACTTGAAGTGGCCAGTGTGTGAAGAGAGATTCGGGATCGAGATC 214
Db      131 GAGGCGACTTGAAGTGGCCAGTGTGTGAAGAGAGATTCGGGATCGAGATC 190
Qy      215 GATTCGGCTCGGGGGCAGAGTGTGATGATTAATGAGACAGTGTGTTT 274
Db      191 TACTCGGCTCGGGGGCAGAGTGTGATGATTAATGAGACAGTGTGTTT 250
Qy      275 TCCAGCTGAGATGGGGCTTCCCTATGAGAAAGATCTCAATTGAGGCAATCGAGAG 334
Db      251 TCCAGCTGAGATGGGGCTTCCCTATGAGAAAGATCTCAATTGAGGCAATCGAGAG 310
Qy      335 GCCAGTATGAGAAACCTTAAGAAATCAACAAGCCGCTCTCCGCTCATCTG 394
Db      311 GCCAGTATGAGAAACCTTAAGAAATCAACAAGCCGCTCTCCGCTCATCTG 370
Qy      395 TGACTGACAGAGCTCGGGTTCCTGCTGTCTGGGGTCAAAACCTTGCTCCCTT 454
Db      371 TGACTGACAGAGCTCGGGTTCCTGCTGTCTGGGGTCAAAACCTTGCTCCCTT 430
Qy      455 GGTCTGCTGGAGTCCCTGCTCTTCCCTACTTAAGTCTTGAAGAAAGAGC 512
Db      431 GGTCTGCTGGAGTCCCTGCTCTTCCCTACTTAAGTCTTGAAGAAAGAGC 488

RESULT 11
US-09-824-787B-67/c
; Sequence 67, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.

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; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 67
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-824-787B-67

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Query Match      55.7%; Score 470.8; DB 10; Length 474;
Best Local Similarity 99.6%; Pred. No. 1.2e-95;
Matches 472; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 236 TTTCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGGCGCAGTAATGAGAAACCTTA 355
DB 474 TTTCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGGCGCAGTAATGAGAAACCTTA 415
QY 356 GAAAAGATCACCAGAGCCGCTCCCTGCTCATCTGTGACTGACAGACACTCTGAGT 415
DB 414 GAAAAGATCACCAGAGCCGCTCCCTGCTCATCTGTGACTGACAGACACTCTGAGT 355
QY 416 TCTCTCTCTGTTCTGAGGCTCAACCTTGTCTCCCTTTGCTGCTGAGAGCTCCGC 475
DB 354 TCTCTCTCTGTTCTGAGGCTCAACCTTGTCTCCCTTTGCTGCTGAGAGCTCCGC 295
QY 476 TGCCCTTTTCCCTCTAGCTCTTAGCAAGAGACCCCTGCGCTCACTTGGCCCTTG 535
DB 294 TGCCCTTTTCCCTCTAGCTCTTAGCAAGAGACCCCTGCGCTCACTTGGCCCTTG 235
QY 536 GGTACAAAGAGAAAGATAGATTCGTTGCTGAGGCTGAGAGAGAGACACTCTCAT 595
DB 234 GGTACAAAGAGAAAGATAGATTCGTTGCTGAGGCTGAGAGAGAGACACTCTCAT 175
QY 596 GAAACCTTCTCAGCAGCACTCATACCCCTTCCAGGGGTAGTGGCCAGAAAGCCAGT 655
DB 174 GAAACCTTCTCAGCAGCACTCATACCCCTTCCAGGGGTAGTGGCCAGAAAGCCAGT 115
QY 656 CCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715
DB 114 CCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 55
QY 716 CCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
DB 54 CCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

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RESULT 12
US-09-824-787B-68/c
; Sequence 68, Application US/09824787B
; Patent No. US2002015547A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 68
; LENGTH: 483
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (248)..(248)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c
; US-09-824-787B-68

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Query Match      54.8%; Score 462.8; DB 10; Length 483;
Best Local Similarity 97.3%; Pred. No. 7.5e-94;
Matches 470; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 279 AGCTGAGAAATGGGGGCTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCA 338
DB 483 AGCTGAGAAATGGGGGCTTTCCCTATGAGAAAGATCTCATTTAGAGCCATCCGAGAGCCA 424
QY 339 GTAATGAGAAACCTTAGAAAAAGATCAACACAGCCGCTCTCCCTGCTCATCTCTGAC 398
DB 423 GTAATGAGAAACCTTAGAAAAAGATCAACACAGCCGCTCTCCCTGCTCATCTCTGAC 364
QY 399 TGACAGAGACTGAGGCTTCTGCTCTGTTCTGAGGCTCAACCTTGTGCTCCCTTTGGTC 458
DB 363 TGACAGAGACTGAGGCTTCTGCTCTGTTCTGAGGCTCAACCTTGTGCTCCCTTTGGTC 304
QY 459 CTGCTGGAGCTCCCTGCTCTCTTCCCTACTTACTGCTCTTACAGAAAGACCTGAC 518
DB 303 CTGCTGGAGCTCCCTGCTCTCTTCCCTACTTACTGCTCTTACAGAAAGACCTGAC 244
QY 519 CTCACTTTGCTGCTTGGGTCAAAAGAAATGAGATTCGTTGCTGAGGCTGAGGAGG 578
DB 243 CTCACTTTGCTGCTTGGGTCAAAAGAAATGAGATTCGTTGCTGAGGCTGAGGAGG 184
QY 579 AGAGAGACACTCTCATGAAACACTTCTCAGCCACTCATCCCTTCCAGGGTAACT 638
DB 183 AGAGAGACACTCTCATGAAACACTTCTCAGCCACTCATCCCTTCCAGGGTAACT 124
QY 639 GCCCAGAAAGCCAGTCACTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
DB 123 GCCCAGAAAGCCAGTCACTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64
QY 699 ATTATTTCTCCCTTACCCAGGCGAATGTCACTATTGAGAGTAAAGTGGCTTACAAAC 758
DB 63 ATTATTTCTCCCTTACCCAGGCGAATGTCACTATTGAGAGTAAAGTGGCTTACAAAC 4
QY 759 ACT 761
DB 3 ACT 1

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RESULT 13
US-09-824-787B-70/c
; Sequence 70, Application US/09824787B
; Patent No. US2002015547A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 70
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (385)..(385)
; OTHER INFORMATION: n is any nucleotide of a, t, g or c

```

US-09-824-787B-70

Query Match 53.4%; Score 451; DB 10; Length 594;

Best Local Similarity 94.0%; Pred. No. 3.5e-91; Mismatches 26; Indels 9; Gaps 7;

Matches 545; Conservative 0; Mismatches 26; Indels 9; Gaps 7;

QY 183 CTGTGAAGAGCAGTATCCGGGCGATCGAGTCGCGGCTCGGGGCGACAGTGCCT 242  
 |||||  
 Db 571 CTGTGAAGAGCAGTATCCGGGCG-TCGAGATGAAT--CGCTCGGGGCGACAGGGTCC 515  
 |||||

QY 243 TTGAGATAGAGATTAATGACAGCTGTGTTCTCAAGCTGAGAAATGGGGGCTTTCCCT 302  
 |||||  
 Db 514 TTGAGATAGAGATTAATGACAGCTGTGCG--TCTCAAGCTGGAATGGGGGCTTTCCCT 457  
 |||||

QY 303 ATGAGAAGATCTCATTTAGAGGCGATCCGAGAGCCAGTAATGAGAAACCTTAGAAGA 362  
 |||||  
 Db 456 ATGAGAAGATCTCATTTAGAGG-CACTCGAAGAGCCAGTAATGAGAAACCTTAGAAGA 398  
 |||||

QY 363 TCACCAACAGCCGTCCTCCGTCGTCATCTGTGATGCAAGGACTCTGGGTTCTGCT 422  
 |||||  
 Db 397 TCACCAACAGCC-NGCTCCCTGCGTCATCTGTGATGCAAGGACTCTGGGT-CTGCT 340  
 |||||

QY 423 CTGTTCGGGGTCCAAACCTTGTCTCCCTTTGCTCTGCTGGAGCTCCCTGCTCT 482  
 |||||  
 Db 339 CTGTTCGGGGTCCAAACCTTGTGT-TCCCTTTGCTCTGCTGGAGCTCCCTGCTCT 281  
 |||||

QY 483 TTCCCTACTTAGCTCCTTAGCAAGAAGACCCTGGCCCTCCACTTGGCCTTTGGGTCAA 542  
 |||||  
 Db 280 TTCCCTACTTAGCTCCTTAGCAAGAAGACCCTGGCCCTCCACTTGGCCTTTGGGTCAA 221  
 |||||

QY 543 AGAAGAAATGAAAGATTCCTGGGCTTGGGGGCGAGAGAGACACTCTCCATGAAACT 602  
 |||||  
 Db 220 AGAAGAAATGAAAGATTCCTGGGCTTGGGGGCGAGAGAGACACTCTCCATGAAACT 161  
 |||||

QY 603 TCTCCAGCCACTATATCCCCCTTCCAGGGTAAGTGCCCGCAAGAACCCAGTCACTCT 662  
 |||||  
 Db 160 TCTCCAGCCACTATATCCCCCTTCCAGGGTAAGTGCCCGCAAGAACCCAGTCACTCT 101  
 |||||

QY 663 TCGGCTCGGTAATACCTGTGATGCGCACAGATTTTATTTATTTCCCTTAACCCAGGGC 722  
 |||||  
 Db 100 TCGGCTCGGTAATACCTGTGATGCGCACAGATTTTATTTATTTCCCTTAACCCAGGGC 41  
 |||||

QY 723 AATGTCACTATTGGCAGTAAGTGCGCTACAAACACTA 762  
 |||||  
 Db 40 AATGTCACTATTGGCAGTAAGTGCGCTACAAACACTA 1  
 |||||

RESULT 14

US-09-824-787B-46/c

Sequence 46, Application US/09824787B

Patent No. US20020155447A1

GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice

APPLICANT: Evans, Elizabeth E.

APPLICANT: Borrello, Melinda A.

TITLE OF INVENTION: A Gene Differentially Expressed in Breast and

FILE REFERENCE: 1821.0040001

CURRENT APPLICATION NUMBER: US/09/824,787B

PRIOR FILING DATE: 2001-04-04

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patent Ver. 2.1

SEO ID NO 46

LENGTH: 456

TYPE: DNA

ORGANISM: Homo sapiens

US-09-824-787B-46

Query Match 53.0%; Score 448; DB 10; Length 456;

Best Local Similarity 100.0%; Pred. No. 1.5e-90; Mismatches 0; Indels 0; Gaps 0;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 GCCATCGAAGAGCCAGTAATGAGAAACCTTAGAAAAGATCACCAAGCCGCTCTCC 382  
 |||||  
 Db 448 GCCATCGAAGAGCCAGTAATGAGAAACCTTAGAAAAGATCACCAAGCCGCTCTCC 389  
 |||||

QY 383 TGGGTCACTCTGACTGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCCAACT 442  
 |||||  
 Db 388 TGGGTCACTCTGACTGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCCAACT 329  
 |||||

QY 443 TGGTCTCCCTTTGGTGTGTGTGGAGCTCCCTGGCTCTTTCCCTACTAGCTCTTA 502  
 |||||  
 Db 328 TGGTCTCCCTTTGGTGTGTGTGGAGCTCCCTGGCTCTTTCCCTACTAGCTCTTA 269  
 |||||

QY 503 GCAAGAGACCTTGCCCTCCACTTTGCTTTGGGTACAAAGAAATAGAAATTCG 562  
 |||||  
 Db 268 GCAAGAGACCTTGCCCTCCACTTTGCTTTGGGTACAAAGAAATAGAAATTCG 209  
 |||||

QY 563 TGGCTTTGGGGGCGAGAGAGACACTCTCATGAACACTTCTCCAGCCACTCATACC 622  
 |||||  
 Db 208 TGGCTTTGGGGGCGAGAGAGACACTCTCATGAACACTTCTCCAGCCACTCATACC 149  
 |||||

QY 623 CTTCCAGGGTAAGTGGCCAGAAAGCCAGTCACTTTGGCTCGGTAATACCTGTC 682  
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 Db 148 CTTCCAGGGTAAGTGGCCAGAAAGCCAGTCACTTTGGCTCGGTAATACCTGTC 89  
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QY 683 TGATGCCACAGATTTTATTTATTTCTCCCTTAACCCAGGGCAATGTAGCTATTGGAGTA 742  
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 Db 88 TGATGCCACAGATTTTATTTATTTCTCCCTTAACCCAGGGCAATGTAGCTATTGGAGTA 29  
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QY 743 AAGTGGCGCTACAAACCTTAATAAAAAA 770  
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 Db 28 AAGTGGCGCTACAAACCTTAATAAAAAA 1  
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RESULT 15

US-09-824-787B-69/c

Sequence 69, Application US/09824787B

Patent No. US20020155447A1

GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice

APPLICANT: Evans, Elizabeth E.

APPLICANT: Borrello, Melinda A.

TITLE OF INVENTION: A Gene Differentially Expressed in Breast and

FILE REFERENCE: 1821.0040001

CURRENT APPLICATION NUMBER: US/09/824,787B

PRIOR FILING DATE: 2001-04-04

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patent Ver. 2.1

SEO ID NO 69

LENGTH: 449

TYPE: DNA

ORGANISM: Homo sapiens

US-09-824-787B-69

Query Match 52.8%; Score 445.8; DB 10; Length 449;

Best Local Similarity 99.6%; Pred. No. 4.6e-90; Mismatches 2; Indels 0; Gaps 0;

Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 317 ATTGAGCCATCCGAAGAGCCAGTAATGAGAAACCTTAGAAAAGATCAACCAAGCCGT 376  
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 Db 449 ATTGAGCCATCCGAAGAGCCAGTAATGAGAAACCTTAGAAAAGATCAACCAAGCCGT 390  
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QY 377 CTTCCCTGCGTACTCTGTGACTGCAAGGACTCTGGGTTCTGCTCTGTTCTGGGGTCC 436  
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 Db 389 CTTCCCTGCGTACTCTGTGACTGCAAGGACTCTGGGTTCTGCTCTGTTCTGGGGTCC 330  
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QY 437 AAACCTTGTCTCCCTTTGTTGTCTGCTGGAGAGTCCCTGCTCTTTCCCTACTTAGC 496  
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 Db 329 AAACCTTGTCTCCCTTTGTTGTCTGCTGGAGAGTCCCTGCTCTTTCCCTACTTAGC 270  
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Qy 497 TCCTTAGCAAGAGACCTGSCCTCCACTTTGGSCCTTTGGGTACAAAGAGGAATAGAAG 556
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Qy 557 ATTCGTGGCCCTTGGGGGAGAGAGACACTTCCATGAACACTTTCAGCCACTC 616
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Db 209 ATTCGTGGCCCTTGGGGGAGAGAGACACTTCCATGAACACTTTCAGCCACTC 150
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Qy 617 ATACCCCTTCCAGGGTAAGTGCCCAAGAAAGCCAGTCACTTGGSCCTGGTAATA 676
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Db 149 ATACCCCTTCCAGGGTAAGTGCCCAAGAAAGCCAGTCACTTGGSCCTGGTAATA 90
    |||||
Qy 677 CCTGTGATGCAAGATTTTATTCTCCCTAACCCAGGGCAATGTCAGCTATTG 736
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Db 89 CCTGTGATGCAAGATTTTATTCTCCCTAACCCAGGGCAATGTCAGCTATTG 30
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Qy 737 GCAGTAAAGTGGCGCTACAAACACTTAAA 765
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Db 29 GCAGTAAAGTGGCGCTACAAACACTTAAA 1
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Search completed: December 18, 2003, 22:36:18  
 Job time : 335 secs

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source
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    /db_xref="taxon:9606"
    /clone="IMAGE:5172146"
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    /lab_host="DH10B"
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BASE COUNT      196 a      232 c      234 g      163 t
ORIGIN
Query Match      86.0%; Score 727; DB 12; Length 825;
Best Local Similarity 98.8%; Pred. No. 2.6e-59;
Matches 764; Conservative 0; Mismatches 5; Indels 4; Gaps 3;

QY 11 CACACCCGGAAGCAGAGGCGCCGAGCGGCGCGATGAGCGGGAGCCGGGCGAG 70
Db 1 CACACCCGGAAGCAGAGG--CCCGAGCGGAGCCGGCGCGATGAGCGGGAGCCGGGCGAG 58

QY 71 ACGTCGTAAGCGCCCTCCCGAGAGAGTGCAGCCGGGAGTGGAGTCCGATGTGTG 130
Db 59 ACGTCGTAAGCGCCCTCCCGAGAGAGTGCAGCCGGGAGTGGAGTCCGATGTGTG 118

QY 131 GAGTACGTGAACCTCGCGCTTGAGAGCGACCTACCTGAGCGTGGCCAGTGTGTGAAG 190
Db 119 GAGTACGTGAACCTCGCGCTTGAGAGCGACCTACCTGAGCGTGGCCAGTGTGTGAAG 178

QY 191 GAGCAGTATCCGGGCGATGAGATGAGTGCAGCTCGCGGGGAGCAGAGTGCCTTGAATA 250
Db 179 GAGCAGTATCCGGGCGATGAGATGAGTGCAGCTCGCGGGGAGCAGAGTGCCTTGAATA 238

QY 251 GAGATTAATGAGACAGTGTGTCTTCCAGCTGAGAAATGGGGCTTCCCTATGAGAAA 310
Db 239 GAGATTAATGAGACAGTGTGTCTTCCAGCTGAGAAATGGGGCTTCCCTATGAGAAA 298

QY 311 GATCTCTTGAAGGCGATCCGAGAGCGATGATGAGAAACCTAGAAAGATGACCAAC 370
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QY 371 AGCGGTCTCCCTGCTATCTGTGACTGACAGAGACTGTGGGTCTCTGTGTCTG 430
Db 359 AGCGGTCTCCCTGCTATCTGTGACTGACAGAGACTGTGGGTCTCTGTGTCTG 418

QY 431 GGGTCCAAACCTGTGTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 490
Db 419 GGGTCCAAACCTGTGTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 478

QY 491 CTTAGTCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550
Db 479 CTTAGTCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538

QY 551 TAGAAGATTCGTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
Db 539 TAGAAGATTCGTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598

QY 611 CACCTATACCCCTCTCCAGAGGTAAGTCCACAGAAAGCCAGTCACTTTCGCTCG 670
Db 599 CACCTATACCCCTCTCCAGAGGTAAGTCCACAGAAAGCCAGTCACTTTCGCTCG 658

QY 671 GTATTACTGTCT-GATGCGCAGATTTATTTATTTCTCCCTTAACCAAGGCAATGCA 729
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QY 730 GCTATTGGCAGT-AAAGTGGCGCTACAAACACTTAAAAA 781
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RESULT 2
BQ960409
LOCUS
DEFINITION
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  AGENCOURT 8945963 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6462483
  5' mRNA sequence.
ACCESSION
  BQ960409
VERSION
  BQ960409.1 GI:22375887
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Organism
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-remail.nih.gov
  Tissue Procurement: ATCC
  CDNA Library Preparation: Rubin Laboratory
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.llnl.gov
  Plate: LCM2652 row: h column: 04
  High quality sequence stop: 626.

FEATURES
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    /db_xref="taxon:9606"
    /clone="IMAGE:6462483"
    /issue_type="epidermoid carcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_101"
    /note="Organ: lung; Vector: pOTB1; Site_1: EcoRI; Site_2:
    XhoI; cDNA made by oligo-dT priming. Directionally cloned
    into EcoRI/XhoI sites using the following 5' adaptor:
    GGCACAG(G). Library constructed by Ling Hong in the
    laboratory of Gerald M. Rubin (University of California,
    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
    Superscript II RT (Life Technologies). Note: this is a
    NIH-MGC Library."

BASE COUNT      168 a      208 c      196 g      155 t      2 others
ORIGIN
Query Match      85.7%; Score 723.8; DB 13; Length 729;
Best Local Similarity 99.5%; Pred. No. 5.6e-59;
Matches 725; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 48 CGATGACGGGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107
Db 1 CGATGACGGGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60

QY 108 GCAGTGGGGTCCGCATCGTGTGAGTACTGTGAACCTTGCGGCTTTCGAGCGACTTACC 167
Db 61 GCAGTGGGGTCCGCATCGTGTGAGTACTGTGAACCTTGCGGCTTTCGAGCGACTTACC 120

QY 168 TGAAGCTGGGCAAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
Db 121 TGAAGCTGGGCAAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 228 GGGGCAAGGTGCTTTGAGATGAGATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 287
Db 181 GGGGCAAGGTGCTTTGAGATGAGATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 288 ATGGGGGCTTTCCCTATGAGAAAGATCTCATTTAGAGCATCCGAGAGCCAGTAATGAG 347

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Db      241 ATGGGGGGCTTCCCTATGAGAAAGATCTATTGAGGCCATCCGAGAGCAGTAATGAG 300
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Qy      348 AAACCTGAGAAAGATCAACCAACAGCCGCTCCCGGCTCATCCGTGACCTGCACAGA 407
        |||
Db      301 AAACCTGAGAAAGATCAACCAACAGCCGCTCCCGGCTCATCCGTGACCTGCACAGA 360
        |||
Qy      408 CTCTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGATCTCCCTTTGGTCTGCTGGA 467
        |||
Db      361 CTCTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGATCTCCCTTTGGTCTGCTGGA 420
        |||
Qy      468 GTCCCTCCCTGCTCTTTCCCTCACTTACCTCTTACCAAGACCTGCTCCACTTT 527
        |||
Db      421 GTCTCCCTCCCTGCTCTTTCCCTCACTTACCTCTTACCAAGACCTGCTCCACTTT 480
        |||
Qy      528 GCCCTTTGGGTCAAGAGAAATGAAATCCCGTGGCTTTGGGGGCGAGAGAGACA 587
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Db      481 GCCCTTTGGGTCAAGAGAAATGAAATCCCGTGGCTTTGGGGGCGAGAGAGACA 540
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Qy      588 CTCTCATGAACACTTCTCCAGCCACCTCATACCCCTTCCAGGGTAAGTCCACAGA 647
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Db      541 CTCTCATGAACACTTCTCCAGCCACCTCATACCCCTTCCAGGGTAAGTCCACAGA 600
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Qy      648 AGCCCACTCACTCTTCCGCTCGGTAAATCTGTCTGATGCCACAGATTTTATTCT 707
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Db      601 AGCCCACTCACTCTTCCGCTCGGTAAATCTGTCTGATGCCACAGATTTTATTCT 660
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Qy      708 CCCCAACCCAGGGAATCTGAGTATTTGGGAGTAAAGTGGGCTTCAAACTAAAAA 767
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Db      661 CCCCAACCCAGGGAATCTGAGTATTTGGGAGTAAAGTGGGCTTCAAACTAAAAA 720
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Qy      768 AAAAAAAAA 776
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Db      721 AAAAAAAAA 729
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DEFINITION 602669368F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4792000 5',
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ACCESSION  Bg705876
VERSION    Bg705876.1 GI:13980659
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 799)
            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
REFERENCE  Contact: Robert Strausberg, Ph.D.
            Email: cgsabbs-remail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizaki
            Yoshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: ILAM10669 row: h column: 17
            High quality sequence stop: 761.
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/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gscgag
); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI/NHGR). National
Institutes of Health. Note: this is a NIH_MGC Library."
BASE COUNT      182 a      230 c      225 g      162 t
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Query Match      85.6%; Score 723; DB 10; Length 799;
Best Local Similarity 98.5%; Pred. No. 6.2e-59;
Matches 740; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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Qy      27  GGGCCGAGCGGAGCGGCGGCGATGAGCGGGGAGCCGGGCGAGACGTCCGTAGCGCCC 86
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Db      14  GGGCCGAGCGGAGCGGCGGCGGATGAGCGGGGAGCCGGGCGAGACGTCCGTAGCGCCC 73
        |||
Qy      87  CTCCGAGAGAGTGAAGCGCGGGGAGTGGGGTCCGATGCTGTGAAGTGAACCTT 146
        |||
Db      74  CTCCGAGAGAGTGAAGCGCGGGGAGTGGGGTCCGATGCTGTGAAGTGAACCTT 133
        |||
Qy      147  GCGGCTTGAAGGAGCACTTCACTGAGCTGCGCAGTGTGAAGAGAGCAGTATCCGGGCA 206
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Db      134  GCGGCTTGAAGGAGCACTTCACTGAGCTGCGCAGTGTGAAGAGAGCAGTATCCGGGCA 193
        |||
Qy      207  TCGAGATGAGTCCGCGCTCGGGGGCAGAGTGCCTTTGAGATGAGATTAATGAGACAGC 266
        |||
Db      194  TCGAGATGAGTCCGCGCTCGGGGGCAGAGTGCCTTTGAGATGAGATTAATGAGACAGC 253
        |||
Qy      267  TGGTGTCTCCAGCTGGAGAAATGGGGCTTTCCCTATGAGAAAGATCTCATTTAGGCA 326
        |||
Db      254  TGGTGTCTCCAGCTGGAGAAATGGGGCTTTCCCTATGAGAAAGATCTCATTTAGGCA 313
        |||
Qy      327  TCCGAAGAGCAGTAATGAGAAACCCATGAAAGATCAACACAGCCGCTCCCTGCG 386
        |||
Db      314  TCCGAAGAGCAGTAATGAGAAACCCATGAAAGATCAACACAGCCGCTCCCTGCG 373
        |||
Qy      387  TCATCTGTGACTGACAGAGACTCTGGGTTCTCTGTTCTGGGGTCCAAACCTTGCT 446
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Db      374  TCATCTGTGACTGACAGAGACTCTGGGTTCTCTGTTCTGGGGTCCAAACCTTGCT 433
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Qy      447  CTCCCTTTGGTCTGCTGCTGGAGGCTCCCTGCTCTTTCCCTACTTAAGTCTTAGCA 506
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Db      434  CTCCCTTTGGTCTGCTGCTGGAGGCTCCCTGCTCTTTCCCTACTTAAGTCTTAGCA 493
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Qy      507  AGAGACCTGAGCTCCACTTGTGCGCTTGGGTACAAAGAGAGATAGAGATTCGCTGGC 566
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Db      494  AGAGACCTGAGCTCCACTTGTGCGCTTGGGTACAAAGAGAGATAGAGATTCGCTGGC 553
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Qy      567  CTTGGGGGAGAGAGAGACACTCTCATGAAACCTTCCAGCCACTATACCCCTT 626
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Db      554  CTTGGGGGAGAGAGAGACACTCTCATGAAACCTTCCAGCCACTATACCCCTT 613
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Qy      627  CCCAGGTAAGTGGCCAGAAAGCCAGTGCATCTTCCGCTCGGTAAATACCTGTGAT 686
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Qy      687  GGCACAGATTTTATTATTCTCCCTTAACCCAGGAGCAATGACCTATTGGCAGTAAGT 746
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RESULT 4
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DEFINITION 602670604F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4793496 5',

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ACCESSION	mRNA sequence.
VERSION	BG707555
KEYWORDS	BG707555.1 GI:13984019
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
TITLE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 778)
COMMENT	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished
	Contact: Robert Strausberg, Ph.D.
	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>
	Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
	Toshiyuki and Piero Carninci (RIKEN)
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>
	Plate: LLNL0673 row: g column: 01
	High quality sequence stop: 764.

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**source**

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/lab_host="DH10B"
/clone_id="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamH; Site 2: SalI-XhoI (gtcggc
); Oligo-dt primed using primer 5'-ttttttttttttttttn-3',
size-selected for average insert size 2.3 kb and
normalized to ROR 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

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Query Match	85.4%	Score 721.8	DB 10	Length 778
Best Local Similarly	99.3%	Pred. No. 8.2e-59		
Matches 756	Conservative	0	Mismatches 2	Indels 3
				Gaps 3

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Db	8	GGAAAGCAGAGGGGCCCGA - GCGAGCGCGCGCGGATGAGAGCGGGAGACCGGGGACAGCGTCG	66
QY	78	TAGAGCCCTCCCGAGGAGGTTCGAGCCGGGACAGTGGGGTCTCGCATCGTGGTGAAGTACT	137
Db	67	TAGAGCCCTCCCGAGGAGGTTCGAGCCGGGACAGTGGGGTCTCGCATCTGGTGAAGTACT	126
QY	138	GTGAACCTTCGCGCTTCGAGCGCATCTA CTTGAGCTGGGCCACAGTGTGTGAAGAGCAGT	197
Db	127	GTGAACCTTCGCGCTTCGAGCGCATCTGAGAGCTGGGCCACAGTGTGTGAAGAGCAGT	186
QY	198	ATCCGGGCAATCGAATCGAGTTCGCGCCTCGGGGGCACAGGTGCTTTGAGATGAGATAA	257
Db	187	ATCCGGGCAATCGAATCGAGTTCGCGCCTCGGGGGCACAGGTGCTTTGAGATGAGATAA	246
QY	258	ATGAGCAGCTGTGTTCCTCAAGCTGGAGAAATGGGGGCTTTCCTATGAGAAAGATCTCA	317
Db	247	ATGAGCAGCTGTGTTCCTCAAGCTGGAGAAATGGGGGCTTTCCTATGAGAAAGATCTCA	306
QY	318	TTGAGGCGCATCGAAGAGCCAGTATGAGAAACCTTAGAAAGATCA CCAACGCCGTC	377
Db	307	TTGAGGCGCATCGAAGAGCCAGTATGAGAAACCTTAGAAAGATCA CCAACGCCGTC	366

QY	378	CTCCCTGGGTATCTCTGTGA-CTGCAACAAGGACTCTGAGGTTCTGCTCTGTTCTGGGGTCCA	437
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QY	438	AACCTTGGTCTCCCTTGGTCTGTGGAGCTCCCTGCTCTTTCCTCCCTACTTAACT	497
Db	427	AACCTTGGTCTCCCTTGGTCTGTGGAGCTCCCTGCTCTTTCCTCCCTACTTAACT	486
QY	498	CCTTAGCAAAAGAACCTTGGGCTTCACITTTGCCCTTTGGGTTCAAAAGAAAGMATTGAA	557
Db	487	CCTTAGCAAAAGAACCTTGGGCTTCACITTTGCCCTTTGGGTTCAAAAGAAAGMATTGAA	546
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Db	547	TTCCGTGGCCTTTGGGGGAGAGAGACATCTTCATGAACACTTTCACAGCCACTCA	606
QY	618	TACCCCTCTCCAGAGGTAAGTGCCACGAAAGCCAGTCACTCTTCGCTCGGTAAATAC	677
Db	607	TACCCCTCTCCAGAGGTAAGTGCCACGAAAGCCAGTCACTCTTCGCTCGGTAAATAC	666
QY	678	CTGTCTGATGCGACAGATTTTATTTATTTCTCCCTAACCCAGGGCAATGTCACTAATTGG	737
Db	667	CTGTCTGATGCGACAGATTTTATTTATTTCTCCCTAACCCA-GGCAATGTCACTAATTGG	725
QY	738	CAGT-AAAGTGGCGCTCAAAACACTAAAAAAAAAAAAAAAAAAAAAAA	777
Db	726	CAGTAAAGGGGCGCTCAAAACACTAAAAAAAAAAAAAAAAAAAAAAA	766

RESULT 5	754 bp	mRNA	linear	EST 24-MAY-2007
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DEFINITION	AGENCOURT 7892547 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158703			
ACCESSION	B0434646			
VERSION	B0434646.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrate; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1 (bases 1 to 754)			
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished			
	Contact: Robert Strausberg, Ph.D.			

Email: [CSGabs-remail.nih.gov](mailto:CSGabs-remail.nih.gov)  
Tissue Procurement: ATCC/CDT/DRP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LHAM1506 row: j column: 16  
High quality sequence stop: 529.

**FEATURES**  
**source**

Query Match	BASE COUNT	ORIGIN
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QY	583	AGACCTCTCATGAACCTTCTTCAGGCACTCATACCCCTCCAGGGTAAGTGGCC	642
Db	589	AGACCTCTCATGAACCTTCTTCAGGCACTCATACCCCTCCAGGGTAAGTGGCC	628
QY	643	ACGAAGCCAGTGCACCTTTCGCTCGGTATATACCTGTGTGATGCCACAGATTTTATTT	702
Db	629	ACGAAGCCAGTGCACCTTTCGCTCGGTATATACCTGTGTGATGCCACAGATTTTATTT	688
QY	703	ATTCTCCCTTAACCCAGGCGCATGTTCAGCTATTGGCAGTAAAGTGGCGCTACAAACACTA	762
Db	689	ATTCTCCCTTAACCCCA-GGCATATGCACCTATTGGCAGTAAAGTGGCGCTACAAACACTA	747
QY	763	AAAAAAAAAAAAA 777	
Db	748	AAAAAAAAAAAAA 762	
RESULT 7	BUI70259	720 bp	mRNA
LOCUS	BUI70259		linear
DEFINITION	AGENCOURT_7909281 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6092434		
ACCESSION	BUI70259		
VERSION	BUI70259.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgi.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cga@bbs-r@mail.nih.gov		
COMMENT	Tissue Procurement: ATCC		
COMMENT	cDNA Library Preparation: Life Technologies, Inc.		
COMMENT	DNA Sequencing by: Agencourt Bioscience Corporation (LML)		
COMMENT	Clone distribution: MGC clone distribution information can be		
COMMENT	found through the I.M.A.G.E. Consortium/LML at:		
COMMENT	http://image.lml.gov		
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	Technologies."		
BASE COUNT	168 a 207 c 191 g 154 t		
ORIGIN			
Query Match	85.1%; Score 719; DB 13; Length 720;		
Best Local Similarity	100.0%; Pred. No. 1.6e-58;		
Matches	719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	60	AGCCGGGAGACGTCGCCGAGCGCCGCCCGGAGAGGTGAGCCGGGCACTGGGGTCC	119
Db	1	AGCCGGGAGACGTCGCCGAGCGCCGCCCGGAGAGGTGAGCCGGGCACTGGGGTCC	60
QY	120	GCATCGTGTGAGTAGTGTGAAACCTTGCAGCTTCGAGGCGACCTACCTGAGCTGGCCA	179
Db	61	GCATCGTGTGAGTAGTGTGAAACCTTGCAGCTTCGAGGCGACCTACCTGAGCTGGCCA	120
QY	180	GTGCTGTGAAGACGATGCCGGGCGATCGAGATGAGTGCAGCTCGGGGCGACAGGTC	239

Db	121	GTGCTGTGAAGAGAGCACTATCCGGGCAATCGAAGTCAAGTGGCGCTCGGGGGGCACAAGTG	180
Oy	240	CCTTTGAGATGAGATTAATGACAGCTGGTGTCTTCCAAAGCTGGAGATGGGGGCTTTC	299
Db	181	CCTTTGAGATGAGATTAATGACAGCTGGTGTCTTCCAAAGCTGGAGATGGGGGCTTTC	240
Oy	300	CCATGAGAAAGATCTCATTTAGAGCCATCCGAAGAGCACTAATGGAAGAAACCTTAATA	359
Db	241	CCATGAGAAAGATCTCATTTAGAGCCATCCGAAGAGCACTAATGGAAGAAACCTTAATA	300
Oy	360	AGATCACCAACAGCCGCTCTCCCTGCTCATCTGTGACTGCACAGGACTCTGGGTTCT	419
Db	301	AGATCACCAACAGCCGCTCTCCCTGCTCATCTGTGACTGCACAGGACTCTGGGTTCT	360
Oy	420	GCTCTGTTCTGGGGTCCAAACCTTGGTCTCCCTTGGTCTGCTGGGAGCTCCCTGGCC	479
Db	361	GCTCTGTTCTGGGGTCCAAACCTTGGTCTCCCTTGGTCTGCTGGGAGCTCCCTGGCC	420
Oy	480	TCCTTCCCTCACTTAGTCTCTTGAGCAAGAGACCCCTGACCTCACTTGGCTTTGGGTA	539
Db	421	TCCTTCCCTCACTTAGTCTCTTGAGCAAGAGACCCCTGACCTCACTTGGCTTTGGGTA	480
Oy	540	CAAGAAGAGATAGAAATTCCTCGTGGGCTGGAGAGAGACACTTCCATGAC	599
Db	481	CAAGAAGAGATAGAAATTCCTCGTGGGCTGGAGAGAGACACTTCCATGAC	540
Oy	600	ACTTCTCCAGCCACTCATACCCCTTCCAGGGTAATGTCGCCAGAAAGCCAGTCCAC	659
Db	541	ACTTCTCCAGCCACTCATACCCCTTCCAGGGTAATGTCGCCAGAAAGCCAGTCCAC	600
Oy	660	TCCTTCCCTGGGTAAATCTGTCTGAGGCCAGATTATTAATTCCTCCCTTAACCCAG	719
Db	601	TCCTTCCCTGGGTAAATCTGTCTGAGGCCAGATTATTAATTCCTCCCTTAACCCAG	660
Oy	720	GGCAATGTCAGCTTTGGCAGTAAAGTGGGCTCAACAACCTAATAAAAAAAAAAAAAA	778
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Frl"
/name="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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NCI CGAP Frl is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
normalized with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_LIB=UI-H-Frl
TAG_TISSUE=Human Lung
Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

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				Gaps	0
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Db	717	CGGGGACAGCGTCCTAGCGCCCTCCCGAGAGGTGAGCCGGGACAGTGGGGTCCGA	658		
QY	123	TCGTGGTGGAGTACTGTGAACCTTCGCGGCTTCGAGGCGACCTACCTGAGCTGGCCAGTG	182		
Db	657	TCGTGGTGGAGTACTGTGAACCTTCGCGGCTTCGAGGCGACCTACCTGAGCTGGCCAGTG	598		
QY	183	CTGTGAAGACACAGTATCCGGGCATCGAGATCGAGTCGCGCTCGGGGCAAGGTCCT	242		
Db	597	CTGTGAAGACACAGTATCCGGGCATCGAGATCGAGTCGCGCTCGGGGCAAGGTCCT	538		
QY	243	TTGAGATGAGATTAATGATGACAGCTGGTGTTCCTCAAGCTGGAGATGGGGCTTTCCT	302		
Db	537	TTGAGATGAGATTAATGATGACAGCTGGTGTTCCTCAAGCTGGAGATGGGGCTTTCCT	478		
QY	303	ATGAGAAAGATCTCATTTAGGCGCATCCGAAAGACAGTAAATGAGAAACCTTAGAAAGA	362		
Db	477	ATGAGAAAGATCTCATTTAGGCGCATCCGAAAGACAGTAAATGAGAAACCTTAGAAAGA	418		
QY	363	TCACCAACAGCCGTCCTCCGCGCATCTGTGACTGACAGACCTGTGGTTCCTGCT	422		
Db	417	TCACCAACAGCCGTCCTCCGCGCATCTGTGACTGACAGACCTGTGGTTCCTGCT	358		
QY	423	CTGTTCGGGGTCCAAACCTTGGTTCCTGCTTGGACCTGGTGGGAGCTCCCGCTCTCT	482		
Db	357	CTGTTCGGGGTCCAAACCTTGGTTCCTGCTTGGACCTGGTGGGAGCTCCCGCTCTCT	298		
QY	483	TTCCCTTACTTAGCTCCTTAGCAAGAGACCCTGGCTTCACTTTGCCCTTTGGGTCA	542		
Db	297	TTCCCTTACTTAGCTCCTTAGCAAGAGACCCTGGCTTCACTTTGCCCTTTGGGTCA	238		
QY	543	AGAGGAATGAGAAATTCGTTGGGCTTGGGGGACAGAGAGACCTCTCCATGAAACT	602		
Db	237	AGAGGAATGAGAAATTCGTTGGGCTTGGGGGACAGAGAGACCTCTCCATGAAACT	178		
QY	603	TTTCAGGCACTCATACCCCTTCCAGGGTAATGGCCAAGAAAGCCAGTCACTCT	662		
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QY	663	TCGGCTGGGTAAATACCTGTCTGATGCCACAGATTTATTATTTCTCCCTTAACCAAGGC	722		
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QY      723 AATGTCAGCTATTGGCAGTAAAGTGCGCTACAACACTAAAAAAAAAAAAA 779
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LOCUS	BQ436860	917 bp	mRNA	linear	EST 24-MAY-2002
DEFINITION	AGENCOURT_7829020 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6056517 5', mRNA sequence.				
ACCESSION	BQ436860				
VERSION	BQ436860.1	GI:21175936			
KEYWORDS	EST.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 917) NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished				
AUTHORS	Contact: Robert Strausberg,	Ph. D.			
TITLE	Email: cgabbs-r@mail.nih.gov				
JOURNAL	Tissue Procurement: DCTD/DRP/Gazdar				
COMMENT	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> plate: LLM13318 row: h column: 22 High quality sequence stop: 650.				

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Query Match	84.2%; Score 711.4; DB 13; Length 917;
Best local Similarity	97.5%; Pred. No. 6,9e-58;
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QY	26 GGGCCCCGAGCGGAGACCCGGCCGCGATGAGCGGGGAGACGTCCTGAGGCCCC 85
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QY 326 ATCCGAGAGCCAGTAAATGAGAAACCTAGAAAAGATCACCAACAGCCGCTCCTGCG 385
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DB 361 GTGATCTGTGATGACAGAGACTCTGGGTTCTGCTCTGTCTGGGGTCCAAACCTTGG 420
QY 446 TCTCCCTTTGCTGCTGTGGAGTCCCTGCTCTTCCCTACTTATGCTCTTGA 505
DB 421 TCTCCCTTTGCTGCTGTGGAGTCCCTGCTCTTCCCTACTTATGCTCTTGA 480
QY 506 AAGAGACCTGAGCTTCCACTTTGGGTACAAAGAAAGATGAAAGATTCCTGCG 565
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QY 566 CTTTGGGGGAGAGAGAGACACTCTCATGACACTTCTCAGCCACTCATACCCCT 625
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RESULT 10
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BG757381
ACCESSION BG757381.1 GI:14068034
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE EST.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-romail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
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for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library.

Query Match 82.2% Score 695; DB 10; Length 705;  
Best Local Similarity 99.3% Pred. No. 2.7e-56;  
Matches 698; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 109 CAGTGGGGTCCGATGTGTGAGATGTAACCTTGGGCTTGAAGGCGACCTA 168
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QY 169 GAGAGTGGCCAGTGTGAGAGAGAGTATCCGGCATTCAGATCGAGCTCGG 228
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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp"

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REFERENCE 1 (bases 1 to 724)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC/CDT/DRP  
 DNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
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 REFERENCE 1 (bases 1 to 759)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: David N. Louis, M.D.  
 DNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
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 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."  
 BASE COUNT 172 a 220 c 212 g 155 t  
 ORIGIN  
 Query Match 82.0%; Score 692.8; DB 10; Length 759;  
 Best Local Similarity 97.4%; Pred. No. 4.1e-56;  
 Matches 736; Conservative 0; Mismatches 17; Indels 3; Gaps 3;  
 Db 30 CCCAGGCGGAGCCGGCCGATGAGCCGGGAGCCGGGGAGAGACTCGTATGCGGCCCTC 89  
 2 CCCAGGCGGAGCCGGCCGATGAGCCGGGAGCCGGGGAGAGACTCGTATGCGGCCCTC 61  
 90 CCCAGGAGTGTGAGCCCGGCGAGTGGGTCCGATCGTGTGAGATCTGTGAACCTTGGC 149  
 Db 62 CCCAGGAGTGTGAGCCCGGCGAGTGGGTCCGATCGTGTGAGATCTGTGAACCTTGGC 121  
 150 GCTTGAAGCGAGCTTACTGAGCTGGCCAGTGTGTGAAGAGACAGTATCCGGGCAATCG 209  
 Db 122 GCTTGAAGCGAGCTTACTGAGCTGGCCAGTGTGTGAAGAGACAGTATCCGGGCAATCG 181

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QY 210 AGATCGAGTCCGCTCGGGGGGCAAGAGTCCCTTTGAGATAGATTAATGACAGCTGG 269
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Db 182 AGATCGAGTCCGCTCGGGGGGCAAGAGTCCCTTTGAGATAGATTAATGACAGCTGG 241
QY 270 TGTTCCTCAAGCTGAGAGATGGGGGCTTTCCCTATGAGAAAGATCTATTGAGCCATCC 329
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Db 242 TGTTCCTCAAGCTGAGAGATGGGGGCTTTCCCTATGAGAAAGATCTATTGAGCCATCC 301
QY 330 GAAGAGCCAGTAAATGAGAAACCTAGAAAGATCAACCAAGCCGCTCCCTGAGCTCA 389
    |||||
Db 302 GAAGAGCCAGTAAATGAGAAACCTAGAAAGATCAACCAAGCCGCTCCCTGAGCTCA 361
QY 390 TCTGTGACTGCAACAGAGACTTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGGTCTC 449
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Db 362 TCTGTGACTGCAACAGAGACTTGGGTTCTGCTCTGTTCTGGGGTCCAAACCTTGGTCTC 421
QY 450 CCTTTGGTCTGCTGAGAGTCCCGCTGCTCTTCCCTTAATTAAGTCTCTTACCAAGA 509
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Db 422 CCTTTGGTCTGCTGAGAGTCCCGCTGCTCTTCCCTTAATTAAGTCTCTTACCAAGA 481
QY 510 GACCCCTGCTCCACTTGGCTTGGGTTCAAAAGAGAAATAGAAATTCGGTGGCTT 569
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Db 482 GACCCCTGCTCCACTTGGCTTGGGTTCAAAAGAGAAATAGAAATTCGGTGGCTT 541
QY 570 GGGGGGCAAGAGAGACACTTCCATGACACTTCTCCAGCCACTCATACCCCTTCCC 629
    |||||
Db 542 GGGGGGCAAGAGAGACACTTCCATGACACTTCTCCAGCCACTCATACCCCTTCCC 601
QY 630 AGGGTAAGTCCCAAGAAAGCCCAAGTCACTTCCCTGGGTAAATCC-TGTGTATGC 688
    |||||
Db 602 AGGGTAAGTCCCAAGAAAGCCCAAGTCACTTCCCTGGGTAAATCC-TGTGTATGC 661
QY 689 CACAGATTTATTTATCTCCCTTAACCAAGGCAATGTCACTAT-TGGCAATGAATG 747
    |||||
Db 662 CACAGA-TTTATTTATTTCTCCCTTAACCAAGGCAATGTCACTAT-TGGCAATGAATG 720
QY 748 GCGCTACAAACACTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 783
    |||||
Db 721 GCGCTACAAACACTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 756

RESULT 13
BF793444 713 bp mRNA linear EST 12-JAN-2001
LOCUS 60254920F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347292 5'
DEFINITION mRNA sequence.
ACCESSION BF793444 GI:12098498
VERSION BF793444.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 713)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Straube, Ph.D.
Email: rstraube@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM9970 row: 9 column: 05
High quality sequence stop: 709.
Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="mRNA"

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/db xref="taxon:9606"
/clone="IMAGE:4347292"
/issue_type="adrenal cortex carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 84"
/Note="Organ: adrenal gland; Vector: pCMV-Sport6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

BASE COUNT 167 a 204 c 187 g 155 t

ORIGIN
Query Match 81.7%; Score 690.4; DB 10; Length 713;
Best Local Similarity 99.7%; Pred. No. 7.2e-56;
Matches 702; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 76 CCGTAGGCCCCCCCCCGAGAGAGTCAAGCCGAGTGGGGTCCGATGCTGTGAGTA 135
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Db 8 CCGTAGGCCCCCCCCCGAGAGAGTCAAGCCGAGTGGGGTCCGATGCTGTGAGTA 67
QY 136 CTGTGAACCTGCGGCTTGAAGGCACTACCTGAGAGTGGCCAGTGTGTAAGAGCA 195
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Db 68 CTGTGAACCTGCGGCTTGAAGGCACTACCTGAGAGTGGCCAGTGTGTAAGAGCA 127
QY 196 GATATCCGGGATGAGATGAGTGGGCTTGGGGGCAAGAGTGCCTTTGATAGAT 255
    |||||
Db 128 GATATCCGGGATGAGATGAGTGGGCTTGGGGGCAAGAGTGCCTTTGATAGAT 187
QY 256 AATGACACGTGCTGTTCTTCCAAAGTGAAGATGGGGCTTCCCTATGAGAAATCT 315
    |||||
Db 188 AATGACACGTGCTGTTCTTCCAAAGTGAAGATGGGGCTTCCCTATGAGAAATCT 247
QY 316 CATTGAGGCGATCCGAAGAGCCAGTATGAGAGAAACCTTAGAAATGACCAACGCCG 375
    |||||
Db 248 CATTGAGGCGATCCGAAGAGCCAGTATGAGAGAAACCTTAGAAATGACCAACGCCG 307
QY 376 TCTCTCCGCTGATCTGTGACTGCAAGAGCTTGGGTTCTGCTCTGTTCTGGGGTC 435
    |||||
Db 308 TCTCTCCGCTGATCTGTGACTGCAAGAGCTTGGGTTCTGCTCTGTTCTGGGGTC 367
QY 436 CAATCCCTGCTCCCTTTGATGCTGCTGGAGCTCCCTGCTCTTCCCTACTTAG 495
    |||||
Db 368 CAATCCCTGCTCCCTTTGATGCTGCTGGAGCTCCCTGCTCTTCCCTACTTAG 427
QY 496 CTCCTTAGCAAGAGAGCCCTGAGCTCACTTGGCTTGGGTACCAAGAGAAATGAA 555
    |||||
Db 428 CTCCTTAGCAAGAGAGCCCTGAGCTCACTTGGCTTGGGTACCAAGAGAAATGAA 487
QY 556 GATTCGCTGCTTGGGGGCAAGAGAGACACTTCCATGAACACTTCTCCAGCCACT 615
    |||||
Db 488 GATTCGCTGCTTGGGGGCAAGAGAGACACTTCCATGAACACTTCTCCAGCCACT 547
QY 616 CATACCCCTTCCCAAGGTAAGGCCAGAAAGCCCAAGTCACTTGGGCTCGGTAAT 675
    |||||
Db 548 CATACCCCTTCCCAAGGTAAGGCCAGAAAGCCCAAGTCACTTGGGCTCGGTAAT 607
QY 676 ACCTGCTGATGCAAGATTTATTTATTTCTCCCTAACCAGAGGCAATGATGAT 735
    |||||
Db 608 ACCTGCTGATGCAAGATTTATTTATTTCTCCCTAACCAGAGGCAATGATGAT 666
QY 736 GCGAGTAAAGTGGCGCTACCAACACTTAAAAAATTTTTTTTTTTTTTTTTTTTT 779
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Db 667 GCGAGTAAAGTGGCGCTACCAACACTTAAAAAATTTTTTTTTTTTTTTTTTTTT 710

RESULT 14
BM981287 711 bp mRNA linear EST 21-FEB-2003
LOCUS BM981287/c
DEFINITION UI-CF-EN1-adh-a-08-0-UI-61 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-adh-a-08-0-UI 3', mRNA sequence.
ACCESSION BM981287
VERSION BM981287.1 GI:19603618

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KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE 1 (bases 1 to 711)  
Normalizaton and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@iowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Source  
1. 711  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EN1-ach-a-08-0-UI"  
/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EN1"  
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Ecor I; Site\_2: Not I;  
UI-CF-EN1 is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an Ecor I adaptor, digested with Not  
I, and cloned directionally into pRTT3-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGT.  
TAG\_LIB=UI-CF-EN1  
TAG\_TISSUE=Human Lung Epithelial Cell lines untreated LPS  
6hr to LPS 24h  
TAG\_SEQ=CTGCTCAGT"

BASE COUNT 154 a 188 c 205 g 164 t

ORIGIN  
Query Match 81.1%; Score 685.4; DB 12; Length 711;  
Best Local Similarity 99.1%; Pred. No. 2.1e-55;  
Matches 689; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 76 CGTACGCCCTTCCTCCGAGAGTGCAGCCGAGGAGTGGGCTCCGATCGTGTGAATA 135  
Db 695 CGTAGCGCCCTCCGAGAGTGCAGCCGAGGAGTGGGCTCCGATCGTGTGAATA 636  
QY 136 CTGTAACCCCTGCGGCTTCGAGGAGTGCAGCCGAGGAGTGGGCTTCGATCGTGTGAATA 195  
Db 635 CTGTAACCCCTGCGGCTTCGAGGAGTGCAGCCGAGGAGTGGGCTTCGATCGTGTGAATA 576  
QY 196 GTATCCGGGATCGATCGAGTGCAGCCGCTCGGGGAGCAGAGTGCCTTTGAGATGAAT 255

Db 575 GTATCCGGGATCGATCGAGTGCAGCCGCTCGGGGAGCAGAGTGCCTTTGAGATGAAT 516  
QY 256 AAATGAGACGTGGTGTCTTCCAGCTGAGAGAAATGGGGCTTTCCCTATGAGAAAGATCT 315  
Db 515 AAATGAGACGTGGTGTCTTCCAGCTGAGAGAAATGGGGCTTTCCCTATGAGAAAGATCT 456  
QY 316 CATTGAGGCGATCCGAGAGCAGTAATGAGAAACCTTAGAAAGATCACCACAGCG 375  
Db 455 CATTGAGGCGATCCGAGAGCAGTAATGAGAAACCTTAGAAAGATCACCACAGCG 396  
QY 376 TCCTCCCTGCTCACTCTGTACTGCACAGAGCTCTGGGTTCTGTCTGTCTGGGGTTC 435  
Db 395 TCCTCCCTGCTCACTCTGTACTGCACAGAGCTCTGGGTTCTGTCTGTCTGGGGTTC 336  
QY 436 CAAACCTTGCTCTCTTTGGTCTGTCTGGGAGCTCCCTGCTCTTTCCCTACTTAG 495  
Db 335 CAAACCTTGCTCTCTTTGGTCTGTCTGGGAGCTCCCTGCTCTTTCCCTACTTAG 276  
QY 496 CTCCTTAGCAAGAGACCCCTGCTCACTTTGCTGCTTGGGTCAAGAGAGATAGAA 555  
Db 275 CTCCTTAGCAAGAGACCCCTGCTCACTTTGCTGCTTGGGTCAAGAGAGATAGAA 216  
QY 556 GATTCCGCTGCTTGGGGGAGAGAGACACTCTCCATGAGACCTTCTCAGCACT 615  
Db 215 GATTCCGCTGCTTGGGGGAGAGAGACACTCTCCATGAGACCTTCTCAGCACT 156  
QY 616 CATACCCCTTCCAGAGGTAAAGTCCCAAGAACCCAGTCACTTTCGCTGGTAT 675  
Db 155 CATACCCCTTCCAGAGGTAAAGTCCCAAGAACCCAGTCACTTTCGCTGGTAT 96  
QY 676 ACCGTGTCGATGCGACAGATTTATTTCTCCCTTAAGCCAGGAGCAATGCACTAT 735  
Db 95 ACCGTGTCGATGCGACAGATTTATTTCTCCCTTAAGCCAGGAGCAATGCACTAT 36  
QY 736 GGCAGTAAGTGGCGCTTCAAAACACTTAAAAA 770  
Db 35 GGCAGTAAGTGGCGCTTCAAAACACTTAAAAA 1

RESULT 15  
BU623706/c  
LOCUS  
DEFINITION BU623706 787 bp mRNA linear EST 23-SEP-2002  
UI-H-FGI-bgi-a-17-0-UI-s1 NCI CGAP FGI Homo sapiens cDNA clone  
UI-H-FGI-bgi-a-17-0-UI 3', mRNA sequence.  
VERSION BU623706.1 GI:23289921  
KEYWORDS EST.  
ORGANISM Homo sapiens (human)  
SOURCE Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE 1 (bases 1 to 787)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-i@mail.nih.gov  
Tissue Procurement: James Martin  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@iowa.edu  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Source  
1. 787  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FGI-bgi-a-17-0-UI"



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 18:35:45 ; Search time 3470 Seconds  
(without alignments)  
9962.143 Million cell updates/sec

Title: US-09-925-301-124

Perfect score: 845  
Sequence: 1 ggcagaggttcacacccgcga.....ggggggggggcccccccccc 845

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pac: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_str: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_ses: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_inv: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pln: \*  
35: em\_hcg\_rtd: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	748	88.5	748	9	BC006006 Homo sapi
2	678.8	80.3	683	6	AX269165 Sequence
3	576	68.2	584	6	AX269179 Sequence
4	532	63.0	532	6	AX269193 Sequence
5	515.8	61.0	571	6	AX269195 Sequence
6	507.8	60.1	528	6	AX269197 Sequence
7	497.8	58.9	501	6	AX269225 Sequence
8	478.2	56.6	518	6	AX269163 Sequence
9	474.8	56.2	488	6	AX269180 Sequence
10	470.8	55.7	474	6	AX269227 Sequence
11	462.8	54.8	483	6	AX269228 Sequence
12	451	53.4	594	6	AX269230 Sequence
13	450.4	53.3	13450	9	AB096612 Homo sapi
14	450.4	53.3	16572	9	AB096614 Homo sapi
15	450.4	53.3	20271	9	AB096613 Homo sapi
16	450.4	53.3	161815	9	AC079199 Homo sapi
17	450.4	53.3	168585	9	AC040933 Homo sapi
18	450.4	53.3	198008	2	AC142197 Homo sapi
19	448	53.0	456	6	AX269206 Sequence
20	445.8	52.8	449	6	AX269229 Sequence
21	444.6	52.6	452	6	AX269203 Sequence
22	444	52.5	444	6	AX269204 Sequence
23	439.4	52.0	30837	9	AY208911 Homo sapi
24	439	52.0	451	6	AX269212 Sequence
25	434	51.4	434	6	AX269210 Sequence
26	434	51.4	434	6	AX269213 Sequence
27	433	51.2	447	6	AX269208 Sequence
28	432.8	51.2	461	6	AX269211 Sequence
29	431.8	51.1	459	6	AX269217 Sequence
30	428.8	50.7	544	6	AX269168 Homo sapi
31	427.6	50.6	508	6	AX269168 Homo sapi
32	426.2	50.4	491	9	HSN308025
33	423	50.1	490	6	AX269166 Sequence
34	421	49.8	421	6	AX269218 Sequence
35	420.6	49.8	427	6	AX269217 Sequence
36	419	49.6	419	6	AX269219 Sequence
37	414.8	48.9	621	6	AX269164 Sequence
38	413	48.9	420	6	AX269181 Sequence
39	407.2	48.2	458	6	AX269202 Sequence
40	403	47.7	403	6	AX269232 Sequence
41	402	47.6	405	6	AX269232 Sequence
42	402	47.6	418	6	AX269221 Sequence
43	400	47.3	404	6	AX156246 Sequence
44	398.8	47.2	454	6	AX269215 Sequence
45	397	47.0	397	6	AX269171 Sequence

# ALIGNMENTS

RESULT 1  
LOCUS BC006006 748 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, similar to RIKEN cDNA 1810046t19 gene, clone  
MGC:14832 IMAGE:4283597, mRNA, complete cds.  
ACCESSION BC006006  
VERSION BC006006.1 GI:13543711  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 748)  
Strausberg, R.  
TITLE Direct Submission

## JOURNAL

Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

## REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC

## COMMENT

CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcddpaxil.stanford.edu](mailto:mcddpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: <http://image.llnl.gov>  
Series: IRAL Plate: 21 Row: h Column: 6  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.

## FEATURES

## source

1..748

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="MGC:14832 IMAGE:4283597"

/tissue\_type="Brain, primitive neuroectodermal"

/clone\_id="NIH\_MGC\_56"

/lab\_host="DH10B"

/note="Vector: pDNR-LIB"

8..355

/codon\_start=1

/product="Similar to RIKEN cDNA 1810046J19 gene"

/protein\_id="AAH06006.1"

/db\_xref="GI:13543712"

/translation="MSGEPQTSVAPEPEVPSGRIYVECPGPFATYLELAS  
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EKITNSRPCTVL"

## CDS

## BASE COUNT

182 a 211 c 200 g 155 t

## ORIGIN

Query Match 88.5%; Score 748; DB 9; Length 748;  
Best Local Similarity 100.0%; Pred. No. 1.2e-135; Indels 0; Gaps 0;  
Matches 748; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

43 GCGCGCATGAGCGGGAGCGGGGAGAGCGTCCGTAGCGCCCTCCCGAGAGGTGCA 102  
1 GCGCGCATGAGCGGGAGCGGGGAGAGCGTCCGTAGCGCCCTCCCGAGAGGTGCA 60  
103 GCGCGCATGAGCGGGAGCGGGGAGAGCGTCCGTAGCGCCCTCCCGAGAGGTGCA 162  
61 GCGCGCATGAGCGGGAGCGGGGAGAGCGTCCGTAGCGCCCTCCCGAGAGGTGCA 120  
163 CTACCTGAGAGTGGCGAGTGTCTGGAAGAGCAATATCCGGGCAATCGAGTGGCG 222  
121 CTACCTGAGAGTGGCGAGTGTCTGGAAGAGCAATATCCGGGCAATCGAGTGGCG 180  
223 CCTCGGGGGGCAAGAGTCTTTGAGATGAGATTAATGAGCAGTGTGTTCTCAAGCT 282  
181 CCTCGGGGGGCAAGAGTCTTTGAGATGAGATTAATGAGCAGTGTGTTCTCAAGCT 240  
283 GAGAAATGGGGGCTTTCTTATGAGAAAGATCTCATTTAGGCGCATCCGAAAGCCAGTAA 342  
241 GAGAAATGGGGGCTTTCTTATGAGAAAGATCTCATTTAGGCGCATCCGAAAGCCAGTAA 300  
343 TGAGAAATCCCTAATAAAGATCAACAAGAGCGGCTCTCCCTGCGTCACTCTGTAAGTCA 402  
301 TGAGAAATCCCTAATAAAGATCAACAAGAGCGGCTCTCCCTGCGTCACTCTGTAAGTCA 360  
403 CAGGACTCTGGGTTCTGTCTGTCTGAGGAGTCCAAACCTTGTCTCCCTTGTGTTCTGTC 462

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Db 361 CAGGACTCTGGGTTCTGTCTGTCTGAGGAGTCCAAACCTTGTCTCCCTTGTGTTCTGTC 420

463 TGGAGTCTCCCTGCTCTTTTCCCTACTACTCTCTTATGCAAGAAGACCTTGCCCTCC 522

421 TGGAGTCTCCCTGCTCTTTTCCCTACTACTCTCTTATGCAAGAAGACCTTGCCCTCC 480

523 ACTTGGCCCTTTGGGTACAAAGAGAAATGAGATTCCTGAGCTTTGGGGGAGAGAG 582

481 ACTTGGCCCTTTGGGTACAAAGAGAAATGAGATTCCTGAGCTTTGGGGGAGAGAG 540

583 AGAAGTCTTCATGAACACTTCTCCAGCACTCATACCCCTTCCAGGGTAAAGTCCC 642

541 AGAAGTCTTCATGAACACTTCTCCAGCACTCATACCCCTTCCAGGGTAAAGTCCC 600

643 ACGAAAGCCAGTCCACTCTTGGCCTCGGTAATACCTGCTGATGCGACAGATTTATTT 702

601 ACGAAAGCCAGTCCACTCTTGGCCTCGGTAATACCTGCTGATGCGACAGATTTATTT 660

703 ATTCTCCCTTACCCAGGAGGAGATGTCAGTATTGGCAGTAAAGTGGCGCTACAAACATA 762

661 ATTCTCCCTTACCCAGGAGGAGATGTCAGTATTGGCAGTAAAGTGGCGCTACAAACATA 720

763 AAAAAAAAAAAAAAAAAAAAAAAAAA 790

721 AAAAAAAAAAAAAAAAAAAAAAAAAA 748

RESULT 2

AX269165 683 bp DNA linear PAT 29-OCT-2001

LOCUS AX269165

DEFINITION Sequence 5 from Patent WO0174859.

ACCESSION AX269165

VERSION AX269165.1 GI:16542081

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Zauderer, M., Evans, E.E. and Borrello, M.A.

A gene differentially expressed in breast and bladder cancer and

encoded polypeptides

Patent: WO 0174859-A 5 11-OCT-2001;

UNIVERSITY OF ROCHESTER (US)

location/Qualifiers

1..683

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 143 a 202 c 187 g 150 t 1 others

ORIGIN

Query Match 80.3%; Score 678.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.4e-122;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

59 GAGCGGGGAGAGAGTCCGTAGCGCCCTCCCGAGAGGTGCAAGCCGGGCAATGGGGTTC 118

1 GAGCGGGGAGAGAGTCCGTAGCGCCCTCCCGAGAGGTGCAAGCCGGGCAATGGGGTTC 60

119 CGATGCTGTGAGTACTGTAACCTCGGAGCTTCCAGGCGAGCTTACTGTAGAGTGGCC 178

61 CGATGCTGTGAGTACTGTAACCTCGGAGCTTCCAGGCGAGCTTACTGTAGAGTGGCC 120

179 AGTGTGTGAAGAGAGTATCCGGGAGTGAATGAGTGGCGCTCGGGGGGAGAGGT 228

121 AGTGTGTGAAGAGAGTATCCGGGAGTGAATGAGTGGCGCTCGGGGGGAGAGGT 180

239 GCGTTGAGTGAAGATTAATGAGAGAGTGTGTTCTCAAGCTGGAAGATGGGGCTTT 298

181 GCGTTGAGTGAAGATTAATGAGAGAGTGTGTTCTCAAGCTGGAAGATGGGGCTTT 240

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QY 299 CCTTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACCTTAGAA 358
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Db 241 CCTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACCTTAGAA 300
|
|
|
QY 359 AAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTGGGTTCC 418
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|
|
Db 301 AAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTGGGTTCC 360
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|
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QY 419 TGCTGTGTTCTGAGGGGTCAGAACCTTGGTCTCCCTTGGTCTGCTGGGAGCTCCCTGTC 478
|
|
|
Db 361 TGCTGTGTTCTGAGGGGTCAGAACCTTGGTCTCCCTTGGTCTGCTGGGAGCTCCCTGTC 420
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QY 479 CTCTTCCCTTACTTAGCTCTTAGCAAGAGACCTTGCGCTCACTTTGCCCCCTT36GT 538
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|
|
Db 421 CTCTGTCCTTACTTAGCTCTTAGCAAGAGACCTTGCGCTCACTTTGCCCCCTT36GT 480
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QY 539 ACAAAGAGAGATAGAAAGATTCCGTGGCCTTGGGGGCGAGAGAGAGACACTTCCATGAA 598
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Db 481 ACAAAGAGAGATAGAAAGATTCCGTGGCCTTGGGGGCGAGAGAGAGACACTTCCATGAA 540
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QY 599 CACTTCTCAGGACCTCTCATACCCCTTCCAGGGGTAAGTGCCCAAGAAAGCCAGTCCA 658
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Db 541 CACTTCTCAGGACCTCTCATACCCCTTCCAGGGGTAAGTGCCCAAGAAAGCCAGTCCA 600
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QY 659 CTCTTCCCTTCCGTAATACCTGTCTGATGCCACAGATTTTATTCTCCCTTAACCA 718
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Db 601 CTCTTCCCTTCCGTAATACCTGTCTGATGCCACAGATTTTATTCTCCCTTAACCA 660
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QY 719 GGGCAATGTCACTTATTGGCAGT 741
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Db 661 GGGCAATGTCACTTATTGGCAGT 683

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RESULT 3
AX269179 584 bp DNA linear PAT 29-OCT-2001
LOCUS AX269179
DEFINITION Sequence 19 from Patent WO0174859.
ACCESSION AX269179
VERSION AX269179.1 GI:16542095
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zauderer,M., Evans,E.E. and Borrelli,M.A.
TITLE A gene differentially expressed in breast and bladder cancer and
JOURNAL encoded polypeptides
PATENT: WO 0174859-A 19 11-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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BASE COUNT 118 a 172 c 171 g 122 t 1 others
ORIGIN
Query Match 68.2%; Score 576; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 3.5e-102;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 GCGGGAGACCGGGGAGAGCTCCCTAGAGCCCTCCGAGAGAGTCCAGCCGGGCAATG 113
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Db 9 GCGGGAGACCGGGGAGAGCTCCCTAGAGCCCTCCGAGAGAGTCCAGCCGGGCAATG 68
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QY 114 GGGTCCGATCGTGTGAGTACTGTGAACCTTGAGGCTTCCAGGCGACCTTACCTGAGC 173
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|
|
Db 69 GGGTCCGATCGTGTGAGTACTGTGAACCTTGAGGCTTCCAGGCGACCTTACCTGAGC 128
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QY 174 TGGCCAGTGTGTGAAGAGAGATCCGGGCGATGAGATCGAGTCCGCGCTCGGGGCA 233
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Db 129 TGGCCAGTGTGTGAAGAGAGATCCGGGCGATGAGATCGAGTCCGCGCTCGGGGCA 188

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QY 234 CAGGTGCTTTGAGATAGATAAATGAGACAGCTGTGTCTCCAGCTGGAGATGGG 293
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Db 189 CAGGTGCTTTGAGATAGATAAATGAGACAGCTGTGTCTCTCAAGCTGGAGATGGG 248
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QY 294 GCTTCCCTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACC 353
|
|
|
Db 249 GCTTCCCTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACC 308
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QY 354 TAGAAAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTGG 413
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|
|
Db 309 TAGAAAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTGG 368
|
|
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QY 414 GTTCTGTCTGTTCTGAGGGTCAGAACCTTGGTCTCCCTTGGTCTGCTGGAGCTCC 473
|
|
|
Db 369 GTTCTGTCTGTTCTGAGGGTCAGAACCTTGGTCTCCCTTGGTCTGCTGGAGCTCC 428
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QY 474 CCGCTCTTTCCCTTACTTAGCTCTTAGCAAGAGACCTTGCGCTTCACTTGGCCTT 533
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Db 429 CCGCTCTTTCCCTTACTTAGCTCTTAGCAAGAGACCTTGCGCTTCACTTGGCCTT 488
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QY 534 TGGTACAAAGAGAGATAGAAAGATTCCGTGGCCTTGGGGGCGAGAGAGACACTTCC 593
|
|
|
Db 489 TGGTACAAAGAGAGATAGAAAGATTCCGTGGCCTTGGGGGCGAGAGAGACACTTCC 548
|
|
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QY 594 ATGAACACTTCTCCAGCCACTCATACCCCTTCC 629
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Db 549 ATGAACACTTCTCCAGCCACTCATACCCCTTCC 584

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RESULT 4
AX269193 532 bp DNA linear PAT 29-OCT-2001
LOCUS AX269193
DEFINITION Sequence 33 from Patent WO0174859.
ACCESSION AX269193
VERSION AX269193.1 GI:16542109
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zauderer,M., Evans,E.E. and Borrelli,M.A.
TITLE A gene differentially expressed in breast and bladder cancer and
JOURNAL encoded polypeptides
PATENT: WO 0174859-A 33 11-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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BASE COUNT 127 a 122 c 156 g 127 t
ORIGIN
Query Match 63.0%; Score 532; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.3e-93;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 ACAGTGTCTTTGAGATAGATAAATGAGACAGCTGTGTCTTCCAGCTGGAGATGGG 292
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|
|
Db 532 ACAGTGTCTTTGAGATAGATAAATGAGACAGCTGTGTCTTCCAGCTGGAGATGGG 473
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QY 293 GCTTCCCTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACC 352
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|
|
Db 472 GCTTCCCTATGAGAAAGATCTCATTGAGGCGCATCCGAGAGCCAGTAATGAGAAACC 413
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QY 353 CTAGAAAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTG 412
|
|
|
Db 412 CTAGAAAGATCACCAGAGCCGCTCTCCCTGCGCATCTGTGACTGACAGAGACTCTG 353
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QY 413 GGTTCGTCTCTGTTCTGAGGGTCAGAACCTTGGTCTCCCTTGGTCTGCTGGAGCTCC 472
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Db      352 GGTTCCTGCTCTGTCTGCGGTCGAACCTTGCTCCCTTTGGTCTCGGAGCTCC 293
QY      473 CCGTCCCTCTTCCCTACTAGCTCCTTAGCAAGAGACCTGGCCCTCACTTTGGCCT 532
Db      292 CCGTCCCTCTTCCCTACTAGCTCCTTAGCAAGAGACCTTGCTCCCTTTGGCCT 233
QY      533 TTGGGTCAAGAAGAAATAGAAATTCGGTGGCTTTGGGGGAGAGAGACACTCTC 592
Db      232 TTGGGTCAAGAAGAAATAGAAATTCGGTGGCTTTGGGGGAGAGAGACACTCTC 173
QY      593 CATGAACACTTCTCCAGCCACTCATACCCCTTCCAGGGTAAAGTCCACGAAGCCC 652
Db      172 CATGAACACTTCTCCAGCCACTCATACCCCTTCCAGGGTAAAGTCCACGAAGCCC 113
QY      653 AGTCCACTCTTCCGCTGGTATACCTGTCTGATGCCACAGATTATTTATCTCCCT 712
Db      112 AGTCCACTCTTCCGCTGGTATACCTGTCTGATGCCACAGATTATTTATCTCCCT 53
QY      713 AACCCAGGCAATGTCAGCTATTGGCAGTAAAGTGGGCTTCAAACTAAA 764
Db      52 AACCCAGGCAATGTCAGCTATTGGCAGTAAAGTGGGCTTCAAACTAAA 1

RESULT 5
AX269195/c 571 bp DNA linear PAT 29-OCT-2001
LOCUS      AX269195 Sequence 35 from Patent WO0174859.
DEFINITION AX269195
ACCESSION  AX269195
VERSION     AX269195.1 GI:16542111
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Zauderer,M., Evans,E.B. and Borrello,M.A.
TITLE       A gene differentially expressed in breast and bladder cancer and
            encoded polypeptides
JOURNAL     Patent: WO 0174859-A 35 11-OCT-2001;
            UNIVERSITY OF ROCHESTER (US)
FEATURES
            Location/Qualifiers
            source
              1..571
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT  133 a 137 c 166 g 131 t 4 others
ORIGIN
Query Match 61.0%; Score 515.8; DB 6; Length 571;
Best Local Similarity 95.8%; Pred. No. 1.8e-90;
Matches 549; Conservative 0; Mismatches 21; Indels 3; Gaps 2;

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Db      273 ACTTAGCTCTTAGCAAGAGACCTTGCCCTCACTTGCCTTTGGTACAAAGAGA 214
QY      550 ATGAGAATTCCTTGCCCTTTGGGGGAGAGAGACACTTCCAGAACACTTCCCG 609
Db      213 ATGAGAATTCCTTGCCCTTTGGGGGAGAGAGACACTTCCAGAACACTTCCCG 154
QY      610 CC-ACCTCATACCCCTTCCAGGGTAAAGTCCAGAAAGCCAGTCCACTTCCCT 668
Db      153 CCAACTCATACCCCTTCCAGGGTAAAGTCCAGAAAGCCAGTCCACTTCCCT 94
QY      669 CGGTAAATCTCTGTATGACACAGATTATTTATTTCTCCCTAACCCAGGCAATGTC 728
Db      93 CGGTAAATCTCTGTATGACACAGATTATTTATTTCTCCCTAACCCAGGCAATGTC 34
QY      729 AGCTATTGGCAGTAAAGTGGGCTTACAAACACT 761
Db      33 AGCTATTGGCAGTAAAGTGGGCTTACAAACACT 1

RESULT 6
AX269197/c 528 bp DNA linear PAT 29-OCT-2001
LOCUS      AX269197 Sequence 37 from Patent WO0174859.
DEFINITION AX269197
ACCESSION  AX269197
VERSION     AX269197.1 GI:16542113
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Zauderer,M., Evans,E.B. and Borrello,M.A.
TITLE       A gene differentially expressed in breast and bladder cancer and
            encoded polypeptides
JOURNAL     Patent: WO 0174859-A 37 11-OCT-2001;
            UNIVERSITY OF ROCHESTER (US)
FEATURES
            Location/Qualifiers
            source
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              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT  127 a 120 c 151 g 126 t 4 others
ORIGIN
Query Match 60.1%; Score 507.8; DB 6; Length 528;
Best Local Similarity 98.9%; Pred. No. 6.6e-89;
Matches 520; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY	601	CTTCTCCAGCCACCTCATACCCCTTCCAGGGGTAAAGGCCAGAAAGCCAGTCACT	660
DB	167	CTTCTCCAGCCACCTCATACCCCTTCCAGGGGTAAAGGCCAGAAAGCCAGTCACT	108
QY	661	CTTGCGCTCGGTAAATACCTGTCTGTATGACAGATTTTATTTATTTCTCCCTTAACCCAG	720
DB	107	CTTGCGCTCGGTAAATACCTGTCTGTATGACAGATTTTATTTATTTCTCCCTTAACCCAG	48
QY	721	GCAATGTACGCTATTGGCAGTAAATGAGCGCTCAACAACACTTAAAA	766
DB	47	GCAATGTACGCTATTGGCAGTAAATGAGCGCTCAACAACAATAAAAA	2
RESULT 7			
LOCUS	AX269225/c	501 bp	DNA
DEFINITION	Sequence 65 from Patent WO0174859.	Linear	PAT 29-OCT-2001
ACCESSION	AX269225		
VERSION	AX269225.1	GI:16542141	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1		
TITLE	Zauderer, M., Evans, F.E. and Borrelli, M.A.		
JOURNAL	A gene differentially expressed in breast and bladder cancer and encoded polypeptides		
FEATURES	Patent: WO 0174859-A 65 11-OCT-2001;		
ORIGIN	UNIVERSITY OF ROCHESTER (US)		
BASE COUNT	122 a 112 c 152 g 115 t		
Query Match	58.9%; Score 497.8; DB 6; Length 501;		
Best Local Similarity	99.6%; Pred. No. 5.8e-87;		
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	263	CAGCTGGTCTCTCCAAAGCTGGAGAAATGGGGCTTTCCCTATGAGAAAGATCTATTGAG	322
DB	501	CAGCTGGTCTCTCCAAAGCTGGAGAAATGGGGCTTTCCCTATGAGAAAGATCTATTGAG	442
QY	323	GCCATCCGAAGAGCCAGTAAATGAGAAACCTAGAAAGATCACCAAGCGCTCC	382
DB	441	GCCATCCGAAGAGCCAGTAAATGAGAAACCTAGAAAGATCACCAAGCGCTCC	382
QY	383	TGCGTCATCTGTGACTGACAGAGACTGTGGGTTCTGCTCTGTTCTGGGGTCCAAACT	442
DB	381	TGCGTCATCTGTGACTGACAGAGACTGTGGGTTCTGCTCTGTTCTGGGGTCCAAACT	322
QY	443	TGCGTCTCCCTTTGGTCTGCTGGGAGCTCCCGCTGCTCTTTCCCTACTTAAAGCTGTTA	502
DB	321	TGCGTCTCCCTTTGGTCTGCTGGGAGCTCCCGCTGCTCTTTCCCTACTTAAAGCTGTTA	262
QY	503	GCAAGAAGAGCCCTGGCTCCCACTTTGGCCCTTTGGGTAACAAGAGAAATGAAGATCCG	562
DB	261	GCAAGAAGAGCCCTGGCTCCCACTTTGGCCCTTTGGGTAACAAGAGAAATGAAGATCCG	202
QY	563	TGGCTTTGGGGGAGAGAGAGACACTTCCTCATGAACATTTCTTCAGCCCACTTATACC	622
DB	201	TGGCTTTGGGGGAGAGAGAGACACTTCCTCATGAACATTTCTTCAGCCCACTTATACC	142
QY	623	CTTTCCTCAAGGTAAAGTGGCCCAAGAAAGCCAGTCACTTTCCGCTGGTAAATCTGTCTC	682
DB	141	CTTTCCTCAAGGTAAAGTGGCCCAAGAAAGCCAGTCACTTTCCGCTGGTAAATCTGTCTC	82
QY	683	TGATGCCACAGATTTTATTTATTTCTCCCTTAACCCAGGGGCAATGTCAAGTATGGGAGTA	742
DB	81	TGATGCCACAGATTTTATTTATTTCTCCCTTAACCCAGGGGCAATGTCAAGTATGGGAGTA	22

[illegible]



ORIGIN

Query Match 54.8%; Score 462.8; DB 6; Length 483;  
 Best Local Similarity 97.3%; Pred. No. 3.7e-80;  
 Matches 470; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

279 AGCTGAGATGGGGCTTCCCTATGAGAAAGATCTCATGAGGCGCATCCGAGGCCA 338  
 483 AGCTGAGATGGGGCTTCCCTATGAGAAAGATCTCATGAGGCGCATCCGAGGCCA 424  
 339 GTAATGAGAAACCTTAGAAAGATCAACAAGCCCTCCCTGCGTCATCTGTGAC 398  
 423 GTAATGAGAAACCTTAGAAAGATCAACAAGCCCTCCCTGCGTCATCTGTGAC 364  
 399 TGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCAAACTTGATCTCCCTTTGGTC 458  
 363 TGACAGAGACTCTGGGTTCTGCTCTGTTCTGGGGTCAAACTTGATCTCCCTTTGGTC 304  
 459 CTGCTGGAGCTCCCTGCTCTCTTCCCTTCTAGCTCTTAGCAAGAGACCTGGC 518  
 303 TTGCTGGAGCTCCCTGCTCTCTTCCCTTCTAGCTCTTAGCAAGAGACCTGGC 244  
 519 CTCCCTTTGCTTGGGTACAAAGAGAAATGAGATTCCTGGGCTTGGGGCGAG 578  
 243 CTCCCTTTGCTTGGGTACAAAGAGAAATGAGATTCCTGGGCTTGGGGCGAG 184  
 579 AGAGAGACTCTCATGAGAACTCTCCAGGACCTCAACCCCTTCCGAGGTAACT 638  
 183 AGAGAGACTCTCATGAGAACTCTCCAGGACCTCAACCCCTTCCGAGGTAACT 124  
 639 GCCCAGAAAGCCAGTCACTCTTCCCTGCTGATACCTGCTGATGCGCAGATTTT 698  
 123 GCCCAGAAAGCCAGTCACTCTTCCCTGCTGATACCTGCTGATGCGCAGATTTT 64  
 699 ATTATTTCTCCCTTAACCCAGGCAATGTCAGCTATTGGCAGTAAAGTGGCGCTTCAAC 758  
 63 ATTATTTCTCCCTTAACCCAGGCAATGTCAGCTATTGGCAGTAAAGTGGCGCTTCAAC 4  
 759 ACT 761  
 3 ACT 1

Db

RESULT 12  
 AX269230/c 594 bp DNA linear PAT 29-OCT-2001  
 LOCUS AX269230  
 DEFINITION Sequence 70 from Patent WO0174859.  
 ACCESSION AX269230  
 VERSION AX269230.1 GI:16542146  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 1 Zauderer M., Evans E.B. and Borrello M.A.  
 A gene differentially expressed in breast and bladder cancer and  
 encoded polypeptides  
 Patent: WO 0174859-A 70 11-OCT-2001;  
 JOURNAL UNIVERSITY OF ROCHESTER (US)  
 TITLE Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 137 a 148 c 171 g 137 t 1 others  
 ORIGIN

Query Match 53.4%; Score 451; DB 6; Length 594;  
 Best Local Similarity 94.0%; Pred. No. 7.7e-78;  
 Matches 545; Conservative 0; Mismatches 26; Indels 9; Gaps 7;

183 CTGTGAAGAGACGATCCGGGCGATCGAGATCGATCGCGGCTCGGGGCGACAGGTGCT 242

Db

571 CTGTGAAGAGACGATCCGGGCG-TCGAGATGAATT--CGCTCGGGGCGACAGGGTGGC 515  
 243 TTGAATAGAGTAATATGACAGCTGTGTTTCCAGCTGGAGAAATGGGGCTTCCCT 302  
 514 TTGAATAGAGTAATATGACAGCTTGGC--TCTCAAACTGGAGAAATGGGGCTTCCCT 457  
 303 ATGAGAAAGATCTCTTGGGCGCATCCGAGAGCCAGTAATGAGAAACCTTAGAAAGA 362  
 456 ATGAGAAAGATCTCTTGGGCGCATCCGAGAGCCAGTAATGAGAAACCTTAGAAAGA 398  
 397 TCACCCACAGCC-NGCTCCCTGCGTCATCTGTGACTGACAGAGACTCTGGGT -CTGCT 340  
 423 CTGTTCTGGGTCCTCAAACTTGTCTCCCTTTGGTCTGCTGGAGCTCCCTGCTCT 482  
 339 CTGTTCTGGGTCCTCAAACTTGTGT--TCCCTTTGGTCTGCTGGAGCTCCCTGCTCT 281  
 483 TTCCCTACTTAACTCTTGAAGAGACCTGGGCTCACTTGGCTTTGGGTACAA 542  
 280 TTCCCTACTTAACTCTTGAAGAGACCTGGGCTCACTTGGCTTTGGGTACAA 221  
 543 AGAAGAAATGAGATTCCTGCTGGGCGCAGAGAGAGACACTCTCCATGAACACT 602  
 220 AGAAGAAATGAGATTCCTGCTGGGCGCAGAGAGAGACACTCTCCATGAACACT 161  
 603 TCTCCAGCACTCTATACCCCTTCCAGGTAAGTCCACGAAAGCCAGTCACTCT 662  
 160 TCTCCAGCACTCTATACCCCTTCCAGGTAAGTCCACGAAAGCCAGTCACTCT 101  
 663 TCGCTGGTAAATCCGTCTGATGCGCAGATTTATTTATTCCTCCCTAACCCAGGC 722  
 100 TCGCTGGTAAATCCGTCTGATGCGCAGATTTATTTATTCCTCCCTAACCCAGGC 41  
 723 AATGTCACTATTGGCAGTAAAGTGGCGCTCAAAACACTA 762  
 40 AATGTCACTATTGGCAGTAAAGTGGCGCTCAAAACACTA 1

Db

RESULT 13  
 AB096612/c 13450 bp DNA linear PRI 21-MAY-2003  
 LOCUS AB096612  
 DEFINITION Homo sapiens DNA, 13kb-normal EcoRI sequence.  
 ACCESSION AB096612  
 VERSION AB096612.1 GI:30962525  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 1 Kuwahara Y., Tanabe C., Ikeuchi T., Aoyagi K., Nishigaki M.,  
 Sakamoto H., Hoshinaga K., Yoshida T., Sasaki H. and Terada M.  
 Presence of novel mechanisms other than the BRB cycles in  
 amplification of human oncogene  
 Unpublished  
 JOURNAL Direct Submission  
 TITLE Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center  
 AUTHORS Research Institute, Genetics Division; Tsukiji 5-1-1, Chuo-ku,  
 Tokyo 104-0045, Japan (E-mail: hksasaki@ncc.ri.nci.go.jp,  
 Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)  
 JOURNAL  
 TITLE Location/Qualifiers  
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 /chromosome="17"  
 /map="17q12"  
 /clone="13kb-normal EcoRI DNA"  
 684..2046

gene

exon /gene="c-ERBB-2"  
684..936  
/gene="c-ERBB-2"  
exon 1078..2046  
/gene="c-ERBB-2"  
/note="3' exon"  
gene 11349..11517  
/gene="GRB7"  
11349..11517  
exon /gene="GRB7"  
BASE COUNT 2748 a 3818 c 3387 g 3496 t 1 others  
ORIGIN

Query Match 53.3%; Score 450.4; DB 9; Length 13450;  
Best Local Similarity 99.8%; Pred. No. 1.6e-77;  
Matches 451; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 312 ATCTCATTTAGAGCCATCCGAGAGCCAGTATATGAGAAACCTTAGAAAGATCACCACCA 371  
DB 2996 AGCTCATTTAGAGCCATCCGAGAGCCAGTATATGAGAAACCTTAGAAAGATCACCACCA 2937  
QY 372 GCGCTCTCCCTGCTGATCTGATGACACAGAGATCTGGGTCTCTGCTGTTCTGG 431  
DB 2936 GCGCTCTCCCTGCTGATCTGATGACACAGAGATCTGGGTCTCTGCTGTTCTGG 2877  
QY 432 GGTCCAAACCTTGGTCTCCCTTTGCTGCTGGAGCTCCCTGCTCTTCCCTTAC 491  
DB 2876 GGTCCAAACCTTGGTCTCCCTTTGCTGCTGGAGCTCCCTGCTCTTCCCTTAC 2817  
QY 492 TTAGCTCTTTAGCAAGAGACCTGAGCTCCACTTTGCGGTACAAAGAGAAAT 551  
DB 2816 TTAGCTCTTTAGCAAGAGACCTGAGCTCCACTTTGCGGTACAAAGAGAAAT 2757  
QY 552 AGAAGATTCCTGCTGCTGGGGGAGAGAGACACTCTTCATGAAACATTTCCAGCC 611  
DB 2756 AGAAGATTCCTGCTGCTGGGGGAGAGAGACACTCTTCATGAAACATTTCCAGCC 2697  
QY 612 ACCGATACCCCTTCCAGGGTATGAGCCACAGAAAGCCAGTCCACTCTTCCCTGAG 671  
DB 2696 ACCGATACCCCTTCCAGGGTATGAGCCACAGAAAGCCAGTCCACTCTTCCCTGAG 2637  
QY 672 TAAATCCTGCTGATGACAGATTTTATTTCTCCCTTAACCCAGGGCAATGTGAGC 731  
DB 2636 TAAATCCTGCTGATGACAGATTTTATTTCTCCCTTAACCCAGGGCAATGTGAGC 2577  
QY 732 TATTGGCAGTAAAGTGGCGCTACCAACACTTA 763  
DB 2576 TATTGGCAGTAAAGTGGCGCTACCAACACTTA 2545

RESULT 14  
AB096614/c 16572 bp DNA linear PRI 21-MAY-2003  
LOCUS Homo sapiens DNA, 16.5kb-T5 rearranged sequence.  
DEFINITION AB096614  
ACCESSION AB096614.1 GI:30962527  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Kuwahara, Y., Tanabe, C., Ikeuchi, T., Aoyagi, K., Nishigaki, M.,  
Sakamoto, H., Hoshinaga, K., Yoshida, T., Saeki, H. and Terada, M.  
TITLE Presence of novel mechanisms other than the BRB cycles in  
amplification of human oncogene  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 16572)  
AUTHORS Sasaki, H.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center  
Research Institute, Genetics Division; Tsukiji 5-1-1, Chuo-Ku,  
Tokyo 104-0045, Japan (E-mail: hkasasaki@gan2.res.ncc.go.jp,

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ORGANISM Homo sapiens  
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TITLE  
JOURNAL

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1  
Kawahara, Y., Tanabe, C., Ikeuchi, T., Aoyagi, K., Nishigaki, M.,  
Sakamoto, H., Hoshinaga, K., Yoshida, T., Sasaki, H. and Terada, M.  
Presence of novel mechanisms other than the BFB cycles in  
amplification of human oncogene  
Unpublished  
2 (bases 1 to 20271)  
Sasaki, H.  
Direct Submission  
Submitted (20-NOV-2002) Hiroki Sasaki, National Cancer Center  
Research Institute, Genetics Division, Tsukiji 5-1-1, Chuo-ku,  
Tokyo 104-0045, Japan (E-mail: hksasaki@gan2.res.ncc.go.jp,  
Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)  
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